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## CRAS

## RESEARCH REQUEST FORM

Scientificiand Technical Information Center

| MCHEV.   |     |
|--|-----|
| Requester's Full Name: K-C-5 RIVINGTAVA Examiner #: 77964 Date: 07/29/2003   | i   |
| Art Unit: 1651 Phone Number 30 605-1196 Serial Number: 10/087,195  | ĺ   |
| Mail Box and Bldg/Room Location: 11 Port Results Format Preferred (circle): PAPER DISK E-MAIL  |     |
| If more than one search is submitted, please prioritize searches in order of need.   |     |
| Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched.   |     |
| Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if |     |
| known. Please attach a copy of the cover sheet, pertinent claims, and abstract.  |     |
| Title of Invention: TRESIMENT OF ALLERGIC RHINITIS   |     |
| Inventors (please provide full names): PARICIA ANNE NUTALL &   |     |
| GUIDO CHRISTIAMN PAESEN  |     |
| Earliest Priority Filing Date: 09/01/1999  |     |
| *For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.  |     |
| Please leaves for Brotein Lequence   |     |
| The AMBLYOM MARY   |     |
| 1=182 MS-HBP1 = SEQ ID#8 TICK BOODHILUS SINT   |     |
| 4 172 FS-HBPL = SEQID#6 ARGUS BAL<br>ANHEBRAEUMAN  |     |
| 4 172 ANHEBRAEUMA  | . : |
| 4 17/ FIST HBPL - SEQIDH7 HAEMAPHYSALISA   |     |
| TXODES81   |     |
| D. RET 6 _ ORNITHODOROS FAL  |     |
| SIMUS  |     |
| ICK = RHIPICEPHALUS EVERTI<br>SANGUINEUS<br>LABORADO WILL ALLERGIC   |     |
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| rmacentate a bupictus  |     |
| YMacentak abopictus  OR (HRODIC OY A CUTE  andersoni  OR (HRODIC OY A CUTE  ALLERSIC RUINITIS OF NIIIS   |     |
| STAFF USE ONLY Type of Search. Vendors and cost where applicable   |     |
| Searcher: Hand NA Sequence (#) STN \$ 182  |     |
| Searcher Phone #: AA.Sequence (#) Dialog   |     |
| Searcher Location: Structure (#) Questel/Orbit   |     |
| Date Searcher Picked Up: 8 / Bibliographic Dr.Link   |     |
| Date Completed: 8/4 Litigation Lexis/Nexis   | -   |
| searcher Prep & Review Time: St 20;57 N Fulltext Sequence Systems  |     |
| Clerical Prep Time: - Patent Family WWW/Internet   |     |
| naline Time: St & 20; ST & 35 Other Other (specify)  |     |
|  |     |

PTO-1590 (8-01)



## STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 99955

TO: Kailash C Srivastava

Location: cm-1/11a12/11b01

Art Unit: 1651

Monday, August 04, 2003

Case Serial Number: 10/087195

From: Susan Hanley

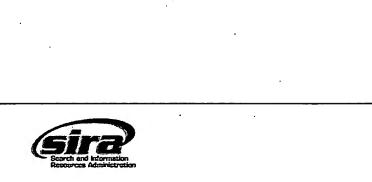
**Location: Biotech-Chem Library** 

CM1 6B05

Phone: 305-4053

susan.hanley@uspto.gov

#### Search Notes





# STIC SEARCH RESULTS FEEDBACK FORM

#### Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

| Voluntary Results Feedback Form   |
|---|
| > I am an examiner in Workgroup: Example: 1610  |
| > Relevant prior art found, search results used as follows:   |
| ☐ 102 rejection   |
| ☐ 103 rejection   |
| ☐ Cited as being of interest.   |
| ☐ Helped examiner better understand the invention.  |
| Helped examiner better understand the state of the art in their technology.   |
| Types of relevant prior art found:  |
| ☐ Foreign Patent(s)   |
| <ul> <li>Non-Patent Literature         <ul> <li>(journal articles, conference proceedings, new product announcements etc.)</li> </ul> </li> </ul> |
| > Relevant prior art <b>not found:</b>  |
| Results verified the lack of relevant prior art (helped determine patentability).   |
| Results were not useful in determining patentability or understanding the invention.  |
| Comments:   |

. DopoiiorsendcompleiediomsioSTC/Blotech-ChamilbianyGMI≒GTic, Desk



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    ANSWER 1 OF 3 REGISTRY COPYRIGHT 2003 ACS on STN
L6
                                                          MS HBP1
    329085-10-1 REGISTRY
RN
    3: PN: WOO116164 TABLE: 1 unclaimed protein (9CI)
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CN
OTHER NAMES:
    3: PN: WOO115719 TABLE: 1 unclaimed protein
CN
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FS
SQL 182
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Sequence | Patent
Source | Reference
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               2 REFERENCES IN FILE CAPLUS (1947 TO DATE)
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       151 KFNEYAVGRE TRDVFTSACL E
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     Unspecified
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CI
SR
     STN Files: CA, CAPLUS, TOXCENTER, USPATFULL
LC
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1 REFERENCES IN FILE CA (1947 TO DATE)
1 REFERENCES IN FILE CAPLUS (1947 TO DATE)

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    ANSWER 3 OF 3 REGISTRY COPYRIGHT 2003 ACS on STN
L6
                                                             FS-HBPI
    329085-08-7 REGISTRY
RN
    1: PN: WOO116164 TABLE: 1 unclaimed protein (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
   1: PN: WOO115719 TABLE: 1 unclaimed protein
FS
    PROTEIN SEQUENCE
SQL 172
PATENT ANNOTATIONS (PNTE):
Sequence | Patent
Source | Reference
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         W02001016164
         |unclaimed
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       151 KFNEYAAGLP VRDVYTSDCL PE
MF
     Unspecified
CI
     MAN
SR
     CA
     STN Files: CA, CAPLUS, TOXCENTER, USPATFULL
LC
               2 REFERENCES IN FILE CA (1947 TO DATE)
               2 REFERENCES IN FILE CAPLUS (1947 TO DATE)
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=> d sqide 128 D. RET 6 L28 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS on STN 200220-35-5 REGISTRY RN Protein D.RET6 (Dermacenter reticularis histamine-binding) (9CI) (CA CN INDEX NAME) FS PROTEIN SEQUENCE SQL 209 SEQ 1 MKMQVVLLLT FVSAALATQA ETTSAKAGEN PLWAHEELLG KYQDAWKSID 51 QGVSVTYVLA KTTYENDTGS WGSQFKCLQV QEIERKEEDY TVTSVFTFRN 101 ASSPIKYYNV TETVKAVFQY GYKNIRNAIE YQVGGGLNIT DTLIFTDGEL 151 CDVFYVPNAD QGCELWVKKS HYKHVPDYCT FVFNVFCAKD RKTYDIFNEE 201 CVYNGEPWL \*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\* MF Unspecified CIMAN SR CA STN Files: CA, CAPLUS LC 2 REFERENCES IN FILE CA (1947 TO DATE)

2 REFERENCES IN FILE CAPLUS (1947 TO DATE)

=> d ibib abs hitstr ind

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L31 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2003 ACS on STN
                            2000:799221 HCAPLUS
 ACCESSION NUMBER:
 DOCUMENT NUMBER:
                            134:55073
                            Vector-host interactions in disease transmission
TITLE:
AUTHOR(S):
                            Nuttall, P. A.; Paesen, G. C.; Lawrie, C. H.; Wang, H.
 CORPORATE SOURCE:
                            CEH Institute of Virology and Environmental
                            Microbiology, Oxford, OX1 3SR, UK
                            Journal of Molecular Microbiology and Biotechnology
SOURCE:
                            (2000), 2(4), 381-386
CODEN: JMMBFF; ISSN: 1464-1801
 PUBLISHER:
                            Horizon Scientific Press
                            Journal; General Review
 DOCUMENT TYPE:
                            English
 LANGUAGE:
      A review with 56 refs. Tick-borne spirochetes include borreliae that cause Lyme disease and relapsing fever in humans. They survive in a
      triangle of parasitic interactions between the spirochete and its
      vertebrate host, the spirochete and its tick vector, and the host and the
      tick. Until recently, the significance of vector-host interactions in the
      transmission of arthropod-borne disease agents has been overlooked.
      However, there is now compelling evidence that the pharmacol. activity of
      tick saliva can have a profound effect on pathogen transmission both from
      infected tick to uninfected host, and from infected host to uninfected tick. The salivary glands of ticks provide a pharmacopoeia of
      anti-inflammatory, anti-hemostatic and anti-immune mols. These include
      bioactive proteins that control histamine, bind Igs, and inhibit the
      alternative complement cascade. The effect of these mols. is to provide a privileged site at the tick-host interface in which borreliae and other
      tick-borne pathogens are sheltered from the normal innate and acquired
      host immune mechanisms that combat infections. Understanding the key
      events at the tick vector-host interface, that promote spirochete
      infection and transmission, will provide a better understanding of the
      epidemiol. and ecol. of these important human pathogens.
      15-0 (Immunochemistry)
      Section cross-reference(s): 12
 ST review immunomodulator tick Borrelia transmission
      Proteins, specific or class
      RL: BOC (Biological occurrence); BSU (Biological study, unclassified);
      BIOL (Biological study); OCCU (Occurrence)
         (Ig-binding proteins; tick vector-host interaction and Borrelia
         transmission in relation to salivary expression of)
 IT
      Complement
         (activation; tick vector-host interaction and Borrelia transmission in
         relation to salivary expression of inhibitors of)
      Proteins, specific or class
 IT
      RL: BOC (Biological occurrence); BSU (Biological study, unclassified);
      BIOL (Biological study); OCCU (Occurrence)
          (histacalins; tick vector-host interaction and Borrelia
         transmission in relation to salivary expression of)
 IT
      Borrelia
      Ixodes
      Lyme disease
      Saliva
          (salivary immunomodulators in tick vector-host interaction and Borrelia
         transmission)
                                   THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS
 REFERENCE COUNT:
                            56
                                   RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
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L5
               8/BI OR 329085-10-1/BI OR 51-45-6/BI)
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L6
                                        PLU=ON HISTACALIN?
L9
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L24
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               L14 OR L15) OR (L18 OR L19)
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=> d ibib abs hitstr 1-14 ind

L32 ANSWER 1 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

2003:492892 HCAPLUS

TITLE:

RNA interference in ticks: a study using

histamine binding protein

dsRNA in the female tick Amblyomma americanum

AUTHOR(S):

Aljamali, M. N.; Bior, A. D.; Sauer, J. R.; Essenberg,

R. C.

CORPORATE SOURCE:

Department Biochemistry and Molecular Biology,

SOURCE:

Oklahoma State University, Stillwater, OK, 74078, USA Insect Molecular Biology (2003), 12(3), 299-305

CODEN: IMBIE3; ISSN: 0962-1075

**PUBLISHER:** 

Blackwell Publishing Ltd.

DOCUMENT TYPE:

Journal

LANGUAGE:

English

RNA interference (RNAi), a gene silencing process, has been recently exploited to det. gene function by degrading specific mRNAs in several eukaryotic organisms. We constructed a double stranded RNA (dsRNA) from a previously cloned putative Amblyomma americanum histamine binding protein (HBP) to test the significance of using this methodol. in the assessment of the function and importance of gene products in ectoparasitic ticks. The female salivary glands incubated in vitro with HBP dsRNA had a significantly lower histamine binding ability. In addn., the injection of HBP dsRNA into the unfed females led both to a reduced histamine binding ability in the isolated salivary glands and to an aberrant tick feeding pattern or host response. Mol. data demonstrated less expression of the HBP mRNA in the RNAi group. Taken together, these results suggest that RNAi might be an important tool for assessing the significance of tick salivary gland secreted proteins modulating responses at the tick-host interface.

INDEXING IN PROGRESS IT

3 (Biochemical Genetics) CC

IT Amblyomma americanum

Protein sequences

cDNA sequences

(rNA interference in ticks, a study using histamine binding protein dsRNA in the female tick Amblyomma americanum)

504653-46-7, GenBank AY246557 IT

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)

(nucleotide sequence; rNA interference in ticks, a study using histamine binding protein dsRNA in the

female tick Amblyomma americanum) 30 · THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS

REFERENCE COUNT:

L32 ANSWER 2 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: DOCUMENT NUMBER:

2002:385176 HCAPLUS 137:229499

TITLE:

Comparison of differentially expressed genes in the

salivary glands of male ticks, Amblyomma americanum

and Dermacentor andersoni

AUTHOR(S):

Bior, Abdelaziz D.; Essenberg, Richard C.; Sauer, John

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

CORPORATE SOURCE:

246 Noble Research Center, Department of Biochemistry and Molecular Biology, Oklahoma State University,

Stillwater, OK, 74078-3035, USA

SOURCE:

Insect Biochemistry and Molecular Biology (2002),

32(6), 645-655 CODEN: IBMBES; ISSN: 0965-1748

PUBLISHER:

Elsevier Science Ltd.

DOCUMENT TYPE: Journal LANGUAGE: English

Genes expressed differentially in the salivary glands of unfed and fed male ticks, Amblyomma americanum (L.), were identified, cloned and sequenced, and some were compared with those expressed in the salivary glands of Dermacentor andersoni. Total protein and RNA increased sixfold in the salivary glands of fed male A. americanum, while in fed male D. andersoni salivary glands, RNA increased approx. 3.5 times. Feeding D. andersoni in the presence of females increased total RNA by 25% over those fed in the absence of females. Complementary DNAs were synthesized from RNA obtained from unfed and fed ticks and amplified using RNA arbitrarily primed polymerase chain reaction (RAP-PCR) with three different primers in sep. reactions. Differential display showed clear banding differences between the fed and the unfed ticks in A. americanum and D. andersoni. Sixty-one cDNA fragments that appeared to be from differentially expressed genes in A. americanum were isolated, cloned and sequenced. Hybridization reactions with labeled cDNA probes confirmed the differential expression of many of the genes in unfed and fed ticks' salivary glands; however, many of the bands contained more than one fragment and some of the fragments isolated from apparently differential bands were not specific. Sequences for 28 of the cDNA fragments (150-600 nucleotides in length) demonstrated similarity to genes in the databases, but nine of these were similar to sequences of unknown function. Some of the gene fragments identified may be important to tick feeding or tick salivary gland physiol., including a histamine-binding protein, an org. ion transporter, an apoptosis inhibitor, a cathepsin-B-like cysteine protease, proteins involved in gene regulation and several proteins involved in protein synthesis. Cross-hybridization of identified cDNAs from A. americanum with cDNA probes synthesized from D. andersoni total RNA did not show significant similarity between the two species.

CC 12-2 (Nonmammalian Biochemistry) Section cross-reference(s): 3

gene expression salivary gland tick Amblyomma Dermacentor male feeding; ST sequence expressed sequence tag male feeding salivary gland tick

IT Amblyomma americanum Dermacentor andersoni Salivary gland Sex

> (comparison of differentially expressed genes in the salivary glands of male ticks. Amblyomma americanum and Dermacentor andersoni)

IT

RL: BSU (Biological study, unclassified); BIOL (Biological study) (comparison of differentially expressed genes in the salivary glands of male ticks, Amblyomma americanum and Dermacentor andersoni)

IT EST (expressed sequence tag)

Gene, animal

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(comparison of differentially expressed genes in the salivary glands of male ticks, Amblyomma americanum and Dermacentor andersoni)

IT cDNA sequences

(for differentially expressed genes in the salivary glands of male ticks, Amblyomma americanum and Dermacentor andersoni)

IT

(meal of; comparison of differentially expressed genes in the salivary

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glands of male ticks, Amblyomma americanum and Dermacentor andersoni)
IT
     Proteins
     RL: BSU (Biological study, unclassified); BIOL (Biological study)
        (salivary gland; comparison of differentially expressed genes in the
        salivary glands of male ticks, Amblyomma americanum and Dermacentor
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     348411-49-4, GenBank BI275513
     RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
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SRIVASTAVA 10/087,195 (Biological study) (nucleotide sequence; comparison of differentially expressed genes in the salivary glands of male ticks, Amblyomma americanum and Dermacentor andersoni) THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS REFERENCE COUNT: 61 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT L32 ANSWER 3 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN 2002:231098 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: 136:383078 A high affinity serotonin- and histamine-binding TITLE: lipocalin from tick saliva Sangamnatdej, S.; Paesen, G. C.; Slovak, M.; Nuttall, AUTHOR(S): P. A. CEH Oxford, Oxford, OX1 3SR, UK CORPORATE SOURCE: Insect Molecular Biology (2002), 11(1), 79-86 SOURCE: CODEN: IMBIE3; ISSN: 0962-1075 PUBLISHER: Blackwell Publishing Ltd. DOCUMENT TYPE: Journal English LANGUAGE: To overcome the inflammatory response in its host, the cattle-feeding, brown ear tick secretes histamine-binding proteins into the feeding site. These proteins are .beta.-barrels
with 2 internal binding sites: a high-affinity (H) site for histamine and a site (L) for which the natural ligand is unknown. Here we report a related protein (SHBP), secreted by a rodent- and cattle-feeding tick, that traps both histamine and serotonin. The histamine-binding H site is well conserved in SHBP, whereas residue changes in the L-like site are consistent with binding of the bulkier serotonin mol. As histamine is a key inflammatory mediator in cattle, while serotonin takes on this role in rodents, the diversification of these tick proteins may reflect host adaptation. 12-1 (Nonmammalian Biochemistry) Section cross-reference(s): 3, 6 Dermacentor saliva serotonin histamine binding lipocalin sequence ST Dermacentor reticulatus IT Feeding Protein sequences Saliva cDNA sequences (high affinity serotonin- and histamine-binding lipocalin sequence and identification from tick saliva) IT RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (lipocalin; high affinity serotonin- and histamine-binding lipocalin sequence and identification from tick saliva) 426310-26-1, Lipocalin (Dermacentor reticulatus) RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (amino acid sequence; high affinity serotonin- and histamine-binding lipocalin sequence and identification from tick saliva) 50-67-9, Serotonin, biological studies 51-45-6, Histamine, biological IT studies RL: BSU (Biological study, unclassified); BIOL (Biological study) (high affinity serotonin- and histamine-binding lipocalin sequence and

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

identification from tick saliva)

381905-30-2, GenBank AF217101

IT

These are all of the cites for the Registry # 5 for FSHBP1 ; 2, MSHBP1 & D. RET 6 ESHBP1

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SRIVASTAVA 10/087,195 # SHBPI
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L5
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L6
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L13
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                 OR 200220-29-7/BI OR 200220-30-0/BI OR 200220-32-2/BI OR
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L26
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1 SEA FILE=REGISTRY ABB=ON PLU=ON L26 AND SQL=209 - D. RETG
L27
L28
              2 SEA FILE=HCAPLUS ABB=ON PLU=ON L28 2 cites for
L29
           STSEAN FILLE HEARING ABBEON PLUEON LESS TORTION 5 C: + e s
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#### => d ibib abs hitstr ind 1-5 130

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L30 ANSWER 1 OF 5 HCAPLUS COPYRIGHT 2003 ACS on STN ACCESSION NUMBER: 2001:168020 HCAPLUS
```

DOCUMENT NUMBER: 134:217189

TITLE: Treatment of allergic rhinitis with proteins from

ticks

INVENTOR(S): Nuttall, Patricia Anne; Paesen, Guido Christiaan

PATENT ASSIGNEE(S): Evolutec Limited, UK SOURCE: PCT Int. Appl., 19 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

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APPLICATION NO.
     PATENT NO.
                         KIND
                               DATE
                                                                    DATE
                                                 WO 2000-GB3287
                                                                    20000824
     WO 2001016164
                          A2
                                20010308
     WO 2001016164
                          Α3
                                20010503
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              CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
              LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
              SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
          RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
              DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
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     EP 1207899
                          A2
             AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
              IE, SI, LT, LV, FI, RO, MK, CY, AL
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     JP 2003508410
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                               20030304
                                                 US 2002-87195
     US 2002193306
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                                20021219
                          A1
PRIORITY APPLN. INFO.:
                                             GB 1999-20673
                                                                 A 19990901
                                             WO 2000-GB3287
                                                                W 20000824
```

AB The invention relates to the discovery that various proteins isolated from ticks are effective in the treatment and prevention of allergic rhinitis. These proteins may most suitably be applied to an effected area and are thus effective to treat this condition and to ameliorate its symptoms. Human subjects were challenged with histamine and then were treated with histamine-binding protein, MS-HBP1.

IT 329085-08-7

RL: PRP (Properties)

(unclaimed protein sequence; treatment of allergic rhinitis with proteins from ticks)

RN 329085-08-7 HCAPLUS

CN 1: PN: WOO116164 TABLE: 1 unclaimed protein (9CI) (CA INDEX NAME)

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

IT 329085-09-8 329085-10-1

RL: PRP (Properties)

(unclaimed sequence; treatment of allergic rhinitis with proteins from ticks)

RN 329085-09-8 HCAPLUS

CN 2: PN: WOO116164 TABLE: 1 unclaimed sequence (9CI) (CA INDEX NAME)

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

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329085-10-1 HCAPLUS
RN
    3: PN: WOO116164 TABLE: 1 unclaimed protein (9CI) (CA INDEX NAME)
CN
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
    ICM C07K014-00
IC
    1-7 (Pharmacology)
CC
    Section cross-reference(s): 12, 15
    allergic rhinitis treatment protein tick; histamine binding protein MSHBP1
ST
     treatment allergic rhinitis
    Proteins, specific or class
TT
    RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
        (D.RET6; treatment of allergic rhinitis with
        proteins from ticks)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
        (FS-HBP1 (female-specific histamine-
        binding protein 1); treatment of allergic
        rhinitis with proteins from ticks)
IT
     Proteins, specific or class
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
     (Uses)
        (FS-HBP2 (female-specific histamine-
        binding protein 2); treatment of allergic
        rhinitis with proteins from ticks)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
        (MS-HBP1 (male-specific histamine-
        binding protein 1); treatment of allergic
        rhinitis with proteins from ticks)
IT
     Nose
        (allergic rhinitis; treatment of allergic rhinitis with proteins from
IT
     Nervous system stimulants
        (antisedatives, medicament also contg.; treatment of allergic rhinitis
        with proteins from ticks)
IT
        (ecto-, histacalin of; treatment of allergic rhinitis with
        proteins from ticks)
IT
     Proteins, specific or class
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
        (histacalins; treatment of allergic rhinitis with proteins
        from ticks)
IT
     Antihistamines
        (medicament also contg.; treatment of allergic rhinitis with proteins
        from ticks)
     Proteins, general, biological studies
IT
     RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
        (of ticks; treatment of allergic rhinitis with proteins from ticks)
IT
     Allergy inhibitors
     Drug delivery systems
     Hay fever
```

```
Mite and Tick
        (treatment of allergic rhinitis with proteins from ticks)
     51-45-6, Histamine, biological studies
IT
    RL: ADV (Adverse effect, including toxicity); BPR (Biological process);
    BSU (Biological study, unclassified); BIOL (Biological study); PROC
        (proteins binding to; treatment of allergic rhinitis with proteins from
        ticks)
IT
     329085-08-7
     RL: PRP (Properties)
        (unclaimed protein sequence; treatment of allergic rhinitis with
        proteins from ticks)
IT
     329085-09-8 329085-10-1
     RL: PRP (Properties)
        (unclaimed sequence; treatment of allergic rhinitis with proteins from
        ticks)
L30 ANSWER 2 OF 5 HCAPLUS COPYRIGHT 2003 ACS on STN
                         2001:167826 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                         134:217188
                         use of histacalin protein for treatment or
TITLE:
                         prevention of conjunctivitis
INVENTOR(S):
                         Nuttall, Patricia Anne; Paesen, Guido Christiaan
                         Evolutec Limited, UK
PATENT ASSIGNEE(S):
                         PCT Int. Appl., 19 pp.
SOURCE:
                         CODEN: PIXXD2
DOCUMENT TYPE:
                         Patent
LANGUAGE:
                         English
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
     PATENT NO.
                      KIND DATE
                                           APPLICATION NO.
                                                            DATE
                            20010308
                                           WO 2000-GB3282
                                                            20000824
    WO 2001015719
                       Α2
                            20010510
     WO 2001015719
                       Α3
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                       T2 20030304
                                           JP 2001-519931
                                                            20000824
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                       A1
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PRIORITY APPLN. INFO.:
                                        GB 1999-20674
                                        WO 2000-GB3282
                                                         W
                                                            20000824
     Various histacalin proteins isolated from ticks are effective in
AB
     the treatment of conjunctivitis. These proteins may most suitably be
     applied topically to an affected area and are effective to ameliorate the
     symptoms of this condition.
     329085-08-7 329085-10-1 329085-11-2
IT
     RL: PRP (Properties)
        (unclaimed sequence; use of histacalin protein for treatment
        or prevention of conjunctivitis)
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329085-08-7 HCAPLUS
RN
    1: PN: WOO116164 TABLE: 1 unclaimed protein (9CI) (CA INDEX NAME)
CN
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
    329085-10-1 HCAPLUS
RN
     3: PN: WOO116164 TABLE: 1 unclaimed protein (9CI) (CA INDEX NAME)
CN
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
    329085-11-2 HCAPLUS
RN
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CN
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
    ICM A61K038-00
IC
     1-7 (Pharmacology)
CC
     Section cross-reference(s): 63
ST
    histacalin antihistamine antiallergic antiinflammatory
     conjunctivitis
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
        (D.RET6; histacalin protein for treatment
        or prevention conjunctivitis)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
        (FS-HBP1; histacalin protein for
        treatment or prevention conjunctivitis)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
     (Uses)
        (FS-HBP2; histacalin protein for
        treatment or prevention conjunctivitis)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
        (MS-HBP1; histacalin protein for
        treatment or prevention conjunctivitis)
IT
     Eye, disease
        (allergic conjunctivitis; histacalin protein for treatment or
        prevention conjunctivitis)
IT
     Eye, disease
        (conjunctivitis: histacalin protein for treatment or
        prevention conjunctivitis)
IT
        (degranulation; histacalin protein for treatment or
        prevention conjunctivitis)
IT
        (ecto-, blood-feeding; histacalin protein for treatment or
        prevention conjunctivitis)
IT
     Allergy inhibitors
     Anti-inflammatory agents
     Antihistamines
     Drug delivery systems
     Mite and Tick
     Protein sequences
        (histacalin protein for treatment or prevention
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conjunctivitis) Proteins, specific or class TT RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (histacalin; histacalin protein for treatment or prevention conjunctivitis) Cell degranulation IT (mast cell; histacalin protein for treatment or prevention conjunctivitis) Mental activity IT (sedation, antisedatives; histacalin protein for treatment or prevention conjunctivitis) IT Drug delivery systems (solns., ophthalmic; histacalin protein for treatment or prevention conjunctivitis) 329085-08-7 329085-10-1 329085-11-2 . IT RL: PRP (Properties) (unclaimed sequence; use of histacalin protein for treatment or prevention of conjunctivitis) L30 ANSWER 3 OF 5 HCAPLUS COPYRIGHT 2003 ACS on STN 1999:374997 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: 131:154999 Tick histamine-binding proteins: isolation, cloning, TITLE: and three-dimensional structure Paesen, G. C.; Adams, P. L.; Harlos, K.; Nuttall, P. AUTHOR(S): A.; Stuart, D. I. Institute of Virology and Environmental Microbiology, CORPORATE SOURCE: Natural Environment Research Council, Oxford, OX1 3SR, Molecular Cell (1999), 3(5), 661-671 SOURCE: CODEN: MOCEFL; ISSN: 1097-2765 Cell Press **PUBLISHER:** Journal DOCUMENT TYPE: English LANGUAGE: High-affinity histamine-binding proteins (HBPs) were discovered in the saliva of Rhipicephalus appendiculatus ticks. Their ability to outcompete histamine receptors indicates that they suppress inflammation during blood feeding. The crystal structure of a histamine-bound HBP, detd. at 1.25 .ANG. resoln., reveals a lipocalin fold novel in contg. two binding sites for the same ligand. The sites are orthogonally arranged and highly rigid and form an internal surface of unusual polar character that complements the physicochem. properties of histamine. As sol. receptors of histamine, HBPs offer a new strategy for controlling histamine-based diseases. 200220-32-2 200220-33-3 200220-34-4 IT RL: PRP (Properties) (amino acid sequence; isolation, cloning, mol. characterization and three-dimensional structure of sex-specific tick histamine-binding proteins) 200220-32-2 HCAPLUS CN Protein FS-HBP1 (Rhipicephalus appendiculatus female-specific histamine-binding) (9CI) (CA INDEX NAME) \*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\* RN 200220-33-3 HCAPLUS Protein FS-HBP2 (Rhipicephalus appendiculatus female-specific CN histamine-binding) (9CI) (CA INDEX NAME) \*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

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200220-34-4 HCAPLUS
RN
    Protein MS-HBP1 (Rhipicephalus appendiculatus male-specific
CN
    histamine-binding) (9CI) (CA INDEX NAME)
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
    6-3 (General Biochemistry)
CC
     Section cross-reference(s): 3, 12
ST
     Rhipicephalus histamine binding protein structure; cDNA sequence tick
     histamine binding protein
    Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BOC (Biological
     occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL
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        histamine-binding proteins)
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     occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL
     (Biological study); OCCU (Occurrence)
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        2); isolation, cloning, mol. characterization and
        three-dimensional structure of sex-specific tick histamine-binding
        proteins)
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     Crystal structure
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     (Properties); BIOL (Biological study); PROC (Process)
        (isolation, cloning, mol. characterization and three-dimensional
        structure of sex-specific tick histamine-binding proteins)
                                  200220-29-7, GenBank U96081 200220-30-0,
IT
     200220-28-6, GenBank U96080
     GenBank U96082
     RL: PRP (Properties)
        (nucleotide sequence; isolation, cloning, mol. characterization and
        three-dimensional structure of sex-specific tick histamine-binding
        proteins)
                         48
                               THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS
REFERENCE COUNT:
```

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 4 OF 5 HCAPLUS COPYRIGHT 2003 ACS on STN ACCESSION NUMBER: 1999:359659 HCAPLUS DOCUMENT NUMBER: 131:28315 Cloning and functions of vasoactive amine-binding TITLE: proteins from ticks INVENTOR(S): Nuttall, Patricia Ann; Paesen, Guido Christian PATENT ASSIGNEE(S): Oxford Vacs Ltd., UK SOURCE: PCT Int. Appl., 84 pp. CODEN: PIXXD2 DOCUMENT TYPE: Patent LANGUAGE: English FAMILY ACC. NUM. COUNT: PATENT INFORMATION: APPLICATION NO. DATE PATENT NO. KIND DATE 19990603 WO 1998-GB3530 19981126 WO 9927104 **A1** W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CA 2309809 AA 19990603 CA 1998-2309809 19981126 AU 9912511 19990615 AU 1999-12511 19981126 A1 EP 1034273 20000913 EP 1998-955786 19981126 A1 AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, RO BR 9815056 20001003 BR 1998-15056 19981126 Α 20020326 JP 2000-522246 19981126 JP 2002508927 . T2 NZ 504753 20021126 NZ 1998-504753 19981126 Α PRIORITY APPLN. INFO.: GB 1997-25046 A 19971126 GB 1998-13917 Α 19980626 WO 1998-GB3530 W 19981126 The present invention relates to histamine and serotonin binding mols. ΑB that possess a binding site with the precise mol. configuration that is necessary to confer on the mol. a high affinity for histamine. The invention includes proteins, peptides and chem. compds. that possess this mol. configuration and that are thus able to bind to histamine with high affinity. These mols. may be used in the regulation of the action of histamine or serotonin, the detection and quantification or histamine or serotonin and in the treatment of various diseases and allergies. The mols. may also be used as components of vaccines directed against blood-sucking ectoparasites. Vasoactive amine binding proteins (VABPs) are provided that specifically bind to vasoactive amines with a dissocn. const. of <10-7 M and which belong to the same protein family as MS-HBP1, FS-HBP1, FS-HBP2 and D.RET6. Thus, 11 VASPs were isolated, and their cDNAs cloned and sequenced, from ticks: FS-HBP1 (female-specific histamine-binding protein 1), FS-HBP2 (female-specific histamine-binding protein 2), MS-HBP1 (male-specific histaminebinding protein 1), and Ra-Res from Rhipicephalus appendiculatus; D.RET6 from Dermacenter reticularis; Av-HBP from Amblyomma variegatum; and 5 related Ih/Bm-HBP

proteins from a mixed Ixodes hexagonus/Boophilus microplus cDNA expression

library. These VASPs possess similar amino acid sequences and predicted secondary structures. The VASPs bind histamine in mammals, and can be used as anti-inflammatory agents to regulate histamine action and to control its pathol. effects. The crystal structure of FS-HBP2 to 2.24 .ANG. resoln. was used to design a synthetic cyclic octapeptide ('Ala-Glu-Ala-Phe-Ala-Glu-Ala-Trp-) with histamine binding activity. 200220-32-2 200220-33-3 200220-34-4 200220-35-5 226891-31-2 226891-34-5 226891-36-7 226891-37-8 226891-38-9 226891-39-0 226891-40-3 RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU

(Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses) (amino acid sequence; cloning and functions of vasoactive amine-binding proteins from ticks)

200220-32-2 HCAPLUS RN

IT

- Protein FS-HBP1 (Rhipicephalus appendiculatus female-specific CN histamine-binding) (9CI) (CA INDEX NAME)
- \*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

200220-33-3 HCAPLUS RN

- Protein FS-HBP2 (Rhipicephalus appendiculatus female-specific CN histamine-binding) (9CI) (CA INDEX NAME)
- \*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

200220-34-4 HCAPLUS RN

- Protein MS-HBP1 (Rhipicephalus appendiculatus male-specific CN histamine-binding) (9CI) (CA INDEX NAME)
- \*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

200220-35-5 HCAPLUS RN

- Protein D.RET6 (Dermacenter reticularis histamine-binding) (9CI) (CA CN INDEX NAME)
- \*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

RN 226891-31-2 HCAPLUS

- Histamine-binding protein Ra-Res (Rhicephalus appendiculatus) (9CI) (CA CN INDEX NAME)
- \*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

RN 226891-34-5 HCAPLUS

- Histamine-binding protein Av-HBP (Amblyomma variegatum) (9CI) (CA INDEX CN
- \*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

RN 226891-36-7 HCAPLUS

- Histamine-binding protein Ih/Bm-HBP1 (Boophilus microplus/Ixodes CN hexagonus) (9CI) (CA INDEX NAME)
- \*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

RN . 226891-37-8 HCAPLUS

- Histamine-binding protein Ih/Bm-HBP2 (Boophilus microplus/Ixodes CN hexagonus) (9CI) (CA INDEX NAME)
- \*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

226891-38-9 HCAPLUS RN

Histamine-binding protein Ih/Bm-HBP3 (Boophilus microplus/Ixodes CN hexagonus) (9CI) (CA INDEX NAME)

113 PAGE BLANK (USPTO)

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

RN 226891-39-0 HCAPLUS

CN Histamine-binding protein Ih/Bm-HBP4 (Boophilus microplus/Ixodes hexagonus) (9CI) (CA INDEX NAME)

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

RN 226891-40-3 HCAPLUS

CN Histamine-binding protein Ih/Bm-HBP5 (Boophilus microplus/Ixodes hexagonus) (9CI) (CA INDEX NAME)

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

IT 226219-91-6

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses) (cloning and functions of vasoactive amine-binding proteins from ticks)

RN 226219-91-6 HCAPLUS

CN Cyclo(L-alanyl-L-alpha.-glutamyl-L-alanyl-L-phenylalanyl-L-alanyl-L-alanyl-L-alanyl-L-tryptophyl) (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-B

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ICM C12N015-21
IC
     ICS C07K014-435; A61K038-17; A61K031-40; A61K031-19; A61K031-66;
          A61K031-35; G01N033-68; A23L001-015; C12N005-10; C12N001-21;
          A01K067-027; C12N015-00
CC
     2-8 (Mammalian Hormones)
     Section cross-reference(s): 1, 3, 6, 12, 75
ST
     vasoactive amine binding protein tick; histamine binding protein tick;
     Rhipicephalus vasoactive amine binding protein; Dermacenter vasoactive
     amine binding protein; Amblyomma vasoactive amine binding protein;
     Boophilus vasoactive amine binding protein; Ixodes vasoactive amine
     binding protein; sequence vasoactive binding protein cDNA tick;
     inflammation inhibitor VASP protein tick
IT
     Proteins, specific or class
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses) (D.RET6; cloning and functions of vasoactive
        amine-binding proteins from ticks)
IT
     Proteins, specific or class
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (FS-HBP1 (female-specific histamine-
        binding protein 1); cloning and functions
        of vasoactive amine-binding proteins from ticks)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (FS-HBP2 (female-specific histamine-
        binding protein 2); cloning and functions
        of vasoactive amine-binding proteins from ticks)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (Ih/Bm-HBP (Ixodes hexagonus/Boophilus microplus histamine-binding
        protein); cloning and functions of vasoactive amine-binding proteins
        from ticks)
     Proteins, specific or class
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (MS-HBP1 (male-specific histamine-
        binding protein 1); cloning and functions
        of vasoactive amine-binding proteins from ticks)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
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     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (VASP (vasoactive amine-binding protein); cloning and functions of
        vasoactive amine-binding proteins from ticks)
     Amines, biological studies
IT
     RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
     (Biological study); PROC (Process)
        (biogenic, vasoactive; cloning and functions of vasoactive
        amine-binding proteins from ticks)
IT
     5-HT antagonists
     Amblyomma variegatum
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Anti-inflammatory agents
    Antihistamines
    Boophilus microplus
    Dermacentor reticulatus
    Ixodes hexagonus
    Mite and Tick
    Molecular cloning
    Rhipicephalus appendiculatus
    Scorpion
    Snake
     Spider
     Transformation, genetic
    Vaccines
        (cloning and functions of vasoactive amine-binding proteins from ticks)
    Fusion proteins (chimeric proteins)
ΙT
    RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL
     (Biological study); PREP (Preparation); USES (Uses)
        (cloning and functions of vasoactive amine-binding proteins from ticks)
     Peptides, biological studies
    RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
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        (cyclic; cloning and functions of vasoactive amine-binding proteins
        from ticks)
IT
     Parasite
        (ecto-; cloning and functions of vasoactive amine-binding proteins from
        ticks)
IT
     cDNA sequences
        (for vasoactive amine-binding proteins from ticks)
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IT
     Plant analysis
        (histamine detn. in; cloning and functions of vasoactive amine-binding
        proteins from ticks)
IT
    Diagnosis
        (mol.; cloning and functions of vasoactive amine-binding proteins from
        ticks)
IT
    Crystal structure
        (of histamine-binding protein FS-HBP2; cloning and
        functions of vasoactive amine-binding proteins from ticks)
IT
    Protein sequences
        (of vasoactive amine-binding proteins from ticks)
IT
        (protein, of histamine-binding protein FS-HBP2;
        cloning and functions of vasoactive amine-binding proteins from ticks)
IT
        (quantification of histamine levels in body fluids; cloning and
        functions of vasoactive amine-binding proteins from ticks)
     200220-32-2 200220-33-3 200220-34-4
IT
     200220-35-5 226891-31-2 226891-34-5
     226891-36-7 226891-37-8 226891-38-9
     226891-39-0 226891-40-3
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (amino acid sequence; cloning and functions of vasoactive amine-binding
        proteins from ticks)
     50-67-9, Serotonin, biological studies
IT
                                             51-45-6, Histamine, biological
               501-75-7, 1-Methylhistamine 644-42-8, 3-Methylhistamine
     RL: ANT (Analyte); BPR (Biological process); BSU (Biological study,
     unclassified); ANST (Analytical study); BIOL (Biological study); PROC
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(Process)
       (cloning and functions of vasoactive amine-binding proteins from ticks)
IT
    226219-91-6
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     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (cloning and functions of vasoactive amine-binding proteins from ticks)
    200220-28-6P
                   200220-29-7P
                                   200220-30-0P
                                                  200220-31-1P
                                                                 226890-87-5P
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                   226890-97-7P
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     226927-07-7P
    RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic
     use); BIOL (Biological study); PREP (Preparation); USES (Uses)
        (nucleotide sequence; cloning and functions of vasoactive amine-binding
       proteins from ticks)
REFERENCE COUNT:
                               THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS
                               RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L30 ANSWER 5 OF 5 HCAPLUS COPYRIGHT 2003 ACS on STN
                         1997:776255 HCAPLUS
ACCESSION NUMBER:
                         128:57765
DOCUMENT NUMBER:
                         Cloning and functions of vasoactive amine-binding
TITLE:
                         proteins from ticks
                         Paesen, Guido Christian; Nuttall, Patricia Ann
INVENTOR(S):
                         Oxford Vacs Ltd., UK; Paesen, Guido Christian;
PATENT ASSIGNEE(S):
                         Nuttall, Patricia Ann
                         PCT Int. Appl., 44 pp.
SOURCE:
                         CODEN: PIXXD2
DOCUMENT TYPE:
                         Patent
                         English
LANGUAGE:
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:
     PATENT NO.
                     KIND DATE
                                          APPLICATION NO. DATE
                      , A2
                            19971127
                                           WO 1997-GB1372 19970519
    WO 9744451
                           19980219
    WO 9744451
                     Α3
        W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
             DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ,
             LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL,
             PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ,
             VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
        RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB,
             GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN,
             ML, MR, NE, SN, TD, TG
                                           CA 1997-2253924 19970519
                      AA
                          19971127
     CA 2253924
     AU 9729071
                      A1
                            19971209
                                           AU 1997-29071
                                                            19970519
                     . B5
     AU 725630
                            20001019
                                           EP 1997-923204
                                                            19970519
     EP 906425
                      Α2
                            19990407
        R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, FI, RO
                            19990803
                                           BR 1997-9101 · 19970519
     BR 9709101
     CN 1225683
                       Α
                            19990811
                                           CN 1997-196317
                                                            19970519
                                                            19970519
                                           NZ 1997-332648
     NZ 332648
                       Α
                            20000526
                                           JP 1997-541799
                                                            19970519
     JP 2000512489
                      T2
                            20000926
                                        GB 1996-10484
                                                      A 19960518
PRIORITY APPLN. INFO.:
                                        GB 1997-7844
                                                         Α
                                                            19970418
                                        WO 1997-GB1372
                                                        W 19970519
     Vasoactive amine binding proteins (VABPs) are provided that specifically
AΒ
     bind to vasoactive amines with a dissocn. const. of <10-7 M and which
```

belong to the same protein family as MS-HBP1,

```
FS-HBP1, FS-HBP2 and D.
    RET6. Thus, 4 VASPs were isolated, and their cDNAs cloned and
    sequenced, from ticks: FS-HBP1 (female-specific
    histamine-binding protein 1),
    FS-HBP2 (female-specific histamine-
    binding protein 2), and MS-
    HBP1 (male-specific histamine-binding
    protein 1) from Rhipicephalus appendiculatus; and
    D.RET6 from Dermacenter reticularis. These 4 VASPs
    possess similar amino acid sequences and predicted secondary structures.
    The VASPs bind histamine in mammals, and can be used as anti-inflammatory
    agents to regulate histamine action and to control its pathol. effects.
    200220-32-2 200220-33-3 200220-34-4
IT
    200220-35-5
    RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (amino acid sequence; cloning and functions of vasoactive amine-binding
        proteins from ticks)
RN
     200220-32-2 HCAPLUS
CN
    Protein FS-HBP1 (Rhipicephalus appendiculatus female-specific
    histamine-binding) (9CI) (CA INDEX NAME)
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
    200220-33-3 HCAPLUS
RN
    Protein FS-HBP2 (Rhipicephalus appendiculatus female-specific
CN
    histamine-binding) (9CI) (CA INDEX NAME)
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
    200220-34-4 HCAPLUS
RN
    Protein MS-HBP1 (Rhipicephalus appendiculatus male-specific
CN
    histamine-binding) (9CI) (CA INDEX NAME)
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
    200220-35-5 HCAPLUS
RN
    Protein D.RET6 (Dermacenter reticularis histamine-binding) (9CI) (CA
CN
    INDEX NAME)
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IC
    ICM C12N015-12
     ICS C12N015-86; A01K067-027; A61K038-17; C12N005-10; G01N033-68;
          C12N015-62; C07K014-435
    2-8 (Mammalian Hormones)
CC
    Section cross-reference(s): 1, 3
    vasoactive amine binding protein tick; histamine binding protein tick;
     Rhipicephalus vasoactive amine binding protein; Dermacenter vasoactive
     amine binding protein; sequence vasoactive binding protein cDNA tick;
     inflammation inhibitor VASP protein tick
IT . Proteins, specific or class
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (D.RET6; cloning and functions of vasoactive
        amine-binding proteins from ticks)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (FS-HBP1 (female-specific histamine-
        binding protein 1); cloning and functions
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of vasoactive amine-binding proteins from ticks)
    Proteins, specific or class
TT
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (FS-HBP2 (female-specific histamine-
        binding protein 2); cloning and functions
        of vasoactive amine-binding proteins from ticks)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (MS-HBP1 (male-specific histamine-
        binding protein 1); cloning and functions
        of vasoactive amine-binding proteins from ticks)
IT
     Proteins, specific or class
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (VASP (vasoactive amine-binding protein); cloning and functions of
        vasoactive amine-binding proteins from ticks)
    Amines, biological studies
IT
     RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
     (Biological study); PROC (Process)
        (biogenic, vasoactive; cloning and functions of vasoactive
        amine-binding proteins from ticks)
    Anti-inflammatory agents
IT
    Antihistamines
     Dermacentor reticulatus
     Mite and Tick
     Molecular cloning
     Rhipicephalus appendiculatus
     Scorpion
     Snake
     Spider
     Transformation, genetic
     Vaccines
        (cloning and functions of vasoactive amine-binding proteins from ticks)
     Fusion proteins (chimeric proteins)
     RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL
     (Biological study); PREP (Preparation); USES (Uses)
        (cloning and functions of vasoactive amine-binding proteins from ticks)
IT
        (ecto-; cloning and functions of vasoactive amine-binding proteins from
        ticks)
IT
     cDNA sequences
        (for vasoactive amine-binding proteins from ticks)
IT
     Protein sequences
        (of vasoactive amine-binding proteins from ticks)
    Body fluid
IT
        (quantification of histamine levels in body fluids; cloning and
        functions of vasoactive amine-binding proteins from ticks)
     200220-32-2 200220-33-3 200220-34-4
IT
     200220-35-5
     RL: BAC (Biological activity or effector, except adverse); BPR (Biological
     process); BSU (Biological study, unclassified); PRP (Properties); THU
     (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
        (amino acid sequence; cloning and functions of vasoactive amine-binding
        proteins from ticks)
     51-45-6, Histamine, biological studies
IT
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RL: ANT (Analyte); BPR (Biological process); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); PROC (Process)

(cloning and functions of vasoactive amine-binding proteins from ticks)
IT 200220-28-6P 200220-29-7P 200220-30-0P 200220-31-1P
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(nucleotide sequence; cloning and functions of vasoactive amine-binding proteins from ticks)

(nucleotide sequence; high affinity serotonin- and histamine-binding

lipocalin sequence and identification from tick saliva)

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L32 ANSWER 4 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:8145 HCAPLUS

DOCUMENT NUMBER: 134:128741

TITLE: Nitrophorins and related antihemostatic lipocalins

from Rhodnius prolixus and other blood-sucking

arthropods

AUTHOR(S): Montfort, William R.; Weichsel, Andrzej; Andersen,

John F.

CORPORATE SOURCE: Department of Biochemistry, University of Arizona,

Tucson, AZ, 85721, USA

SOURCE: Biochimica et Biophysica Acta (2000), 1482(1-2),

110-118

CODEN: BBACAQ; ISSN: 0006-3002

PUBLISHER: Elsevier Science B.V. DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

A review, with 53 refs. Recent gene sequence and crystal structure detns. of salivary proteins from several blood-sucking arthropods have revealed an unusual evolutionary relationship: many such proteins derive their functions from lipocalin protein folds. Many blood-sucking arthropods have independently evolved the ability to overcome a host organism's means of preventing blood loss (called hemostasis). Most blood feeders have proteins that induce vasodilation, inhibit blood coagulation, and reduce inflammation, but do so by distinctly different mechanisms. Despite this diversity, in many cases the antihemostatic activities in such organisms reside in proteins with lipocalin folds. Thirteen such lipocalins are described in this review, with a particular focus on the heme-contg. nitrophorins from R. prolixus, which transport nitric oxide, sequester histamine, and disrupt blood coagulation. Also described are the anti-platelet compds. RPAI, moubatin, and pallidipin from R. prolixus, Ornithodoros moubata, and Triatoma pallidipennis; the antithrombin protein triabin from T. pallidipennis; and the tick histamine binding proteins from Rhipicephalus appendiculatus.

CC 12-0 (Nonmammalian Biochemistry) Section cross-reference(s): 6

ST review blood sucking arthropod nitrophorin lipocalin

IT Arthropod (Arthropoda)

(blood-sucking; nitrophorins and related antihemostatic lipocalins from Rhodnius prolixus and other blood-sucking arthropods)

IT Proteins, specific or class

RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)

(lipocalins; nitrophorins and related antihemostatic lipocalins from Rhodnius prolixus and other blood-sucking arthropods)

IT Rhodnius prolixus

Salivary gland

(nitrophorins and related antihemostatic lipocalins from Rhodnius prolixus and other blood-sucking arthropods)

IT Proteins, specific or class

RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)

(nitrophorins; nitrophorins and related antihemostatic lipocalins from Rhodnius prolixus and other blood-sucking arthropods)

REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L32 ANSWER 5 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

2001:8143 HCAPLUS

DOCUMENT NUMBER:

134:128740
Tick histamine-binding

TITLE:

proteins: lipocalins with a second binding

cavity

AUTHOR(S):

Paesen, Guido C.; Adams, Peter L.; Nuttall, Patricia

A.; Stuart, David L.

CORPORATE SOURCE:

CEH Institute of Virology and Environmental

Microbiology, Oxford, OX1 3SR, UK

SOURCE:

Biochimica et Biophysica Acta (2000), 1482(1-2),

92-101

CODEN: BBACAQ; ISSN: 0006-3002

PUBLISHER: DOCUMENT TYPE:

Elsevier Science B.V. Journal; General Review

LANGUAGE: English

AB A review, with 26 refs. Tick histamine-binding

proteins (HBPs) are lipocalins with 2 binding pockets. One of these binds histamine with a high affinity and is found at the position expected from other lipocalins, adjacent to the .OMEGA.-loop at the open-end of the .beta.-barrel. A 2nd binding cavity, which is a low-affinity site for histamine in 1 of the HBPs, is located at the end of the barrel that is closed off in other lipocalins. To create the 2nd site, the closed-end region has undergone a major reconstruction. Typical lipocalin characteristics, such as the 310 helix and a structural cluster of highly conserved residues, have been lost, while an .alpha.-helix now shields the cavity from the exterior. The prominence of acidic residues

in the binding pockets is another distinctive characteristic of HBPs. Whereas most lipocalins have highly hydrophobic binding cavities designed to bind lipophilic compds., HBPs have evolved to trap cationic,

hydrophilic mols.

CC 12-0 (Nonmammalian Biochemistry)
Section cross-reference(s): 6

ST review tick histamine binding protein

IT Proteins, specific or class

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)

(histamine-binding; tick histamine-binding

proteins)

IT Mite and Tick

(tick histamine-binding proteins)

REFERENCE COUNT:

THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L32 ANSWER 6 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1994:236350 HCAPLUS

DOCUMENT NUMBER:

120:236350

TITLE:

Purification of histamine receptor proteins from

detergent-solubilized human peripheral blood

mononuclear cells

AUTHOR(S):

Warlow, Robert S.; Rajasekariah, Poornima; Lambert, Paul; Morgan, Janelle; Dao, Lan Phuong; Bernard,

Claude C. A.; Walls, Ronald S.

CORPORATE SOURCE:

Immunology Department, Concord Repatriation Hospital,

Sydney, Australia

SOURCE:

Biochemistry (1994), 33(16), 4800-11

CODEN: BICHAW; ISSN: 0006-2960

DOCUMENT TYPE:

Journal

LANGUAGE:

Enalish

Histamine is released from mast cells and basophils by either immunol. or nonimmunol. mechanisms. Histamine, which is the most potent short acting mediator released from these cells, exerts its diverse biol. actions by binding to cell surface histamine receptors. The authors report the affinity purifn. of histamine receptor proteins from Triton X-100 solubilized peripheral human blood mononuclear cells which include lymphocytes and monocytes. Three different designs of histamine affinity columns were constructed; all three resulted in the same material being eluted. This consisted of bands which on SDS-PAGE after boiling and redn. had the following mol. wts.: 193K, 84K, 58K, 48K, 37K, and 16K. The most abundant bands were of mol. wts. 193K, 48K, and 16K, and these were disulfide bonded together to form a high mol. wt. complex. The 58K band was present in lower amts. than the others, and in only a few fractions. It had the same mol. wt. as the dimeric form of histamine methyltransferase which is present in small amts. in mononuclear cells and may therefore have copurified. The histamine binding proteins described in this report were purified by conventional affinity chromatog., rather than by an expression cloning approach which obviates the use of any protein chem. Consequently, the authors had the advantage of being able to verify the histamine binding specificity of the purified proteins directly and with several independent assays as follows. The histamine binding specificity of all three columns was established by specific elution with histamine, by preabsorption of crude cell ext. with excess free histamine prior to column application, and by comparison with control columns. Independent detn. of the binding specificity, using a radioreceptor dot blot assay, of the eluate contg. only the 193K, 48K, and 16K disulfide-linked subunits confirmed that the purified material bound specifically to [3H]histamine and that a 300-500-fold degree of purifn. from tissue ext. had been obtained. Following cell surface radioreceptor crosslinking of radiolabeled histamine to intact mononuclear cells, the 16K band was detected, indicating it to be the ligand-binding subunit for histamine. These same three proteins were purified from T lymphocyte and monocytoid cell lines, indicating that both lymphocyte and monocyte subsets of mononuclear cells express these proteins. The trimol. structure, consisting of 193K, 48K, and 16K subunits appears to be a novel histamine cell surface receptor protein complex as the mol. wts. of the 193K, 48K, and 16K bands bore no relation to the predicted mol. wts. of the recently expression cloned H1 receptor gene derived from bovine adrenal and H2 receptor gene derived from human parietal cells; this may reflect receptor heterogeneity within a tissue, between tissues, and/or between species.

cc2-2 (Mammalian Hormones)

histamine receptor mononuclear cell purifn characterization; affinity ST chromatog histamine receptor mononuclear cell; lymphocyte histamine receptor purifn characterization; monocyte histamine receptor purifn characterization; structure histamine receptor mononuclear cell

IT Monocyte

(histamine receptors of human, purifn. and characterization of)

IT Cell membrane

(histamine receptors of, of human blood mononuclear cells, purifn. and characterization of)

Conformation and Conformers IT

Disulfide group

(of histamine receptors, of human blood mononuclear cells)

IT Lymphocyte

(T-cell, histamine receptors of human, purifn. and characterization of)

IT Chromatography, column and liquid

(affinity, of histamine receptors, of human blood mononuclear cells)

```
IT
    Receptors
     RL: BIOL (Biological study)
        (histaminic, of blood mononuclear cells, of human, purifn. and
        characterization of)
IT
    Leukocvte
        (mononuclear, histamine receptors of human, purifn. and
        characterization of)
     51-45-6P, Histamine, biological studies
IT
     RL: BIOL (Biological study); PREP (Preparation)
        (receptor binding of, after purifn. from human blood mononuclear cells)
L32 ANSWER 7 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                         1991:421847 HCAPLUS
DOCUMENT NUMBER:
                         115:21847
                         Histaglobulin and changes in conjunctival structure in
TITLE:
                         vernal conjunctivitis
                         Volokhovskaya, Z. P.; Kadyrova, M. Ya.
AUTHOR(S):
                         Turk. NII Glazn. Bolezn., Ashkhabad, USSR
CORPORATE SOURCE:
                         Zdravookhranenie Turkmenistana (1990), (10), 15-18
SOURCE:
                         CODEN: ZDTUAB; ISSN: 0513-8736
DOCUMENT TYPE:
                         Journal
LANGUAGE:
                         Russian
     The histochem. effects of 2-3-wk course treatment with histaglobin
     (histamine-binding globulin) on eye conjunctiva were studied in humans
     suffering from spring allergic conjunctivitis. The treatment decreased
     infiltration with basophils responsible for amine release and allergic
     symptoms.
     1-7 (Pharmacology)
     Section cross-reference(s): 15
     allergic conjunctivitis histochem histaglobulin histamine binding;
    histamine binding protein allergic
     conjunctivitis histochem
     Proteins, specific or class
IT
     RL: BIOL (Biological study)
        (histamine-binding, allergic spring conjunctivitis histochem. response
        to treatment with, in humans)
     Eye, disease or disorder
IT
        (vernal conjunctivitis, histaglobin treatment effects on histochem. of.
        in humans)
L32 ANSWER 8 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                         1981:404871 HCAPLUS
DOCUMENT NUMBER:
                         95:4871
                         Histamine binding proteins
TITLE:
                         separated from human serums by the chromatographic
                         method
                         Chachaj, Wladyslaw; Bartecka, Zuzanna; Malolepszy,
AUTHOR(S):
CORPORATE SOURCE:
                         Dep. Intern. Dis., Inst. Intern. Dis., Wroclaw, Pol.
                         Archivum Immunologiae et Therapiae Experimentalis
SOURCE:
                         (1980), 28(6), 947-51
                         CODEN: AITEAT; ISSN: 0004-069X
DOCUMENT TYPE:
                         Journal
                         Enalish
LANGUAGE:
     Human serum proteins were bound on and eluted from Sepharose-polylysine-
     histamine column. Thus obtained protein fraction was referred to as HBP (
     histamine-binding protein). HBPs were examd.
     for the ability to bind histamine by biol. method applied to isolated
     guinea pig intestine. Chromatog. sepns. were run on DEAE cellulose column
     to obtain HBPs which are directly responsible for histamine-binding
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activity. The results suggest that human serum contains 3 HBP fractions.
     One of them was identified as orosomucoid, and the 2 remaining ones seem
     to be glycoproteins belonging to .alpha.1 globulin group.
CC
     15-1 (Immunochemistry)
     histamine binding protein chromatog
ST
IT
     Blood serum
        (histamine-binding proteins of)
IT
     Allergy
        (histamine-binding proteins of blood
        serum in relation to)
     51-45-6, biological studies
IT
     RL: BIOL (Biological study)
        (proteins binding, of blood serum)
L32 ANSWER 9 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN
                         1979:536384 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                         91:136384
                         Application of affinity chromatography in binding of
TITLE:
                         histamine to serum proteins
                         Bartecka, Z.; Chachaj, W.; Malepszy, J.
AUTHOR(S):
                         Inst. Intern. Med., Med. Acad. Wroclaw, Wroclaw, Pol.
CORPORATE SOURCE:
                         Agents and Actions (1979), 9(1), 35-7
SOURCE:
                         CODEN: AGACBH; ISSN: 0065-4299
DOCUMENT TYPE:
                         Journal
                         English
LANGUAGE:
     Serum histamine (I)-binding proteins (HBP) were isolated by affinity
     chromatog. on polylysine-Sepharose 4B-immobilized histamine (II) and
     characterized by electrophoresis. Dialyzed serum proteins were incubated
     with a suspension of carrier II for 2 h at 37.degree., and the carrier
     then was packed in a column, washed with 0.9% NaCl to remove unbound
     proteins, and eluted with 0.2M EDTA and 6M urea to remove HBP.
     Polyacrylamide gel electrophoresis in the presence of 0.2% Na dodecyl
     sulfate sepd. 8 HBP fractions with mol. wts. in the range 80,000-350,000.
     A bioassay with isolated guinea pig intestine was used to det. I and to
     study its inactivation at various HBP concns.
     9-2 (Biochemical Methods)
CC
     serum histamine binding protein sepn;
ST
     affinity chromatog histamine binding protein
IT
     Blood analysis
        (histamine-binding proteins affinity.
        chromatog. in)
     Chromatography, column and liquid
TT
        (affinity, of histamine-binding proteins)
IT
     Proteins
     RL: PROC (Process)
        (histamine-binding, affinity chromatog. of, of blood serum)
     9012-36-6D, reaction product with poly-L-lysine
IT
     RL: ANST (Analytical study)
        (histamine immobilization on, for histamine-binding
        proteins affinity chromatog.)
     51-45-6, biological studies
IT
     RL: BIOL (Biological study)
        (proteins binding, affinity chromatog. of, of blood serum)
L32 ANSWER 10 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN
                         1978:35352 HCAPLUS
ACCESSION NUMBER: -
DOCUMENT NUMBER:
                         88:35352
                         Histamine and serotonin content in patients with newly
TITLE:
                         identified tuberculosis of the lungs complicated by
                         nonspecific endobronchitis
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Shesterina, M. V.; Mikhailova, Yu. V.; Andrzheyuk, N.
AUTHOR(S):
                          I.; Elistratova, N. A.
                          Mosk. Nauchno-Issled. Inst. Tuberk., Moscow, USSR
CORPORATE SOURCE:
SOURCE:
                          Problemy Tuberkuleza (1977), (9), 36-9
                          CODEN: PRTUAX; ISSN: 0032-9533
DOCUMENT TYPE:
                          Journal
LANGUAGE:
                          Russian
     In 50 adult patients with tuberculosis and nonspecific endobronchitis, the
     blood levels of histamine and serotonin increased and those of
     histamine-binding protein decreased 2-, 1.5-
     and 5-fold, resp., in the patients without microflora in the bronchi and
     1.4-, 1.5-, and 2-fold, resp., in the patients with addnl. microflora in the bronchi as compared with those of normal subjects. After treatment with antibiotics and antihistamines or corticosteroids, the levels usually
     normalized.
CC
     14-1 (Mammalian Pathological Biochemistry)
     histamine serotonin blood tuberculosis; bronchitis microorganism
     tuberculosis; protein serum histamine binding endobronchitis
IT
        (blood compn. in, endobronchitis in relation to)
     Proteins
     RL: BIOL (Biological study)
        (histamine-binding, of blood in tuberculosis and endobronchitis)
IT
     Bronchi
        (disease, endobronchitis, blood compn. in tuberculosis in relation to)
                                     51-45-6, biological studies
     50-67-9, biological studies
     RL: BIOL (Biological study)
        (of blood, in tuberculosis and endobronchitis)
L32 ANSWER 11 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                          1975:81859 HCAPLUS
DOCUMENT NUMBER:
                          82:81859
TITLE:
                          Histamine-serum protein bond
                          Kochman, S.; Jalouzot, R.; Maujean, A.; Cazabat, A.;
AUTHOR(S):
                          Dubois de Montreynaud, J. M.
                          Serv. Pneumophisiologie, Cent. Hosp. Univ., Reims, Fr.
CORPORATE SOURCE:
SOURCE:
                          Nouvelle Presse Medicale (1974), 3(30), 1883
                          CODEN: NPMDAD: ISSN: 0301-1518
DOCUMENT TYPE:
                          Journal
                          French
LANGUAGE:
     Gel chromatog, of normal human serum on a histamine-fixed. CNBr-activated
     Sepharose 4B column adsorbed the histaminoplexic compd. of the serum.
     Elution with 6M quanidine-HCl yielded a protein (max. uv absorbance at280
     nm). Na dodecyl sulfate-polyacrylamide gel electrophoresis showed only 2
     bands. Thus, the presence of a histamine-binding
     protein in blood serum is confirmed.
     6-3 (General Biochemistry)
     blood serum protein histamine binding
ST
IT
     Proteins
     RL: BIOL (Biological study)
        (blood-serum, histamine binding by)
IT
     51-45-6, biological studies
     RL: BIOL (Biological study)
        (protein binding, of blood serum)
L32 ANSWER 12 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN
                          1974:502483 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                          81:102483
                          New aspects of histaminopexy
TITLE:
AUTHOR(S):
                          Lonovics, J.; Gecse, A.; Karady, S.
```

CORPORATE SOURCE:

Inst. Pathophysiol., Univ. Sch. Med., Szeged, Hung.

SOURCE:

Archives Internationales de Physiologie et de

Biochimie (1974), 82(1), 41-7 CODEN: AIPBAY; ISSN: 0003-9799

DOCUMENT TYPE: LANGUAGE: Journal English

AB The mechanism of formation and release of histaminopexic peptide was studied in the rat. Detns. were carried out with plasma and serum which were first subjected to gel filtration on Sephadex G-25. Agarose gel electrophoresis was used to sep. polypeptides, and free histamine (I) was assayed with an atropinized guinea pig ileum suspended in Tyrode's soln. Whereas I-binding activity of plasma was in the protein fraction, in serum it was in the peptide region; after papain digestion, results with plasma were similar to those with serum. Adrenalectomy caused loss of I-binding activity, unless rats were treated with prednisolone succinate. The I-binding peptide probably released from albumin by a papainlike action during blood coagulation. Adrenal cortex function is needed for maintenance of I-binding activity.

C 13-13 (Mammalian Biochemistry)

ST histamine binding protein blood; adrenal histamine binding protein

IT Proteins

RL: BIOL (Biological study)

(histamine binding, blood-plasma, regulation of)

IT Corticosteroids, biological studies

RL: BIOL (Biological study)

(histamine-binding peptide of blood serum in response to)

IT Peptides, biological studies RL: BIOL (Biological study)

(histamine-binding, of blood serum, regulation of)

IT 2920-86-7

RL: BIOL (Biological study)

(histamine-binding peptide of blood serum in response to)

IT 51-45-6, biological studies RL: BIOL (Biological study)

(peptide of blood serum binding of, regulation of)

L32 ANSWER 13 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1972:111092 HCAPLUS

DOCUMENT NUMBER:

76:111092

TITLE:

Histamine-binding property of human serum

AUTHOR(S):

Gecse, A.; Lonovics, J.; Szekeres, L.; Zsilinszky, E.;

West, G. B.

CORPORATE SOURCE:

Sch. Med., Univ. Szeged, Szeged, Hung.

SOURCE:

Journal of Pharmacy and Pharmacology (1972), 24(1),

70-1

CODEN: JPPMAB; ISSN: 0022-3573

DOCUMENT TYPE:

Journal

LANGUAGE:

English

AB Expts. performed on serum from healthy adult humans indicated that the albumin fraction in some way binds histamine, whereas all other fractions of the plasma were lacking in such activity. When the fraction contg. 96% of albumin was digested with papain, and then passed through Sephadex G-25, the histamine-binding activity moved to the polypeptide region of the plasma. All the low-mol.-wt. polypeptide portion had been released from the albumin during coagulation, or by papain digestion. Plasma albumin or serum peptide from blood of 8 allergic patients (generalized dermatoses) lacked histamine-binding activity, indicating that lack of a histaminopexic substance may be involved in the pathogenesis of allergic diseases.

## SRIVASTAVA 10/087,195

CC 13 (Mammalian Biochemistry) blood histamine binding protein ST Allergy IT (histamine binding by albumins of blood serum in) Albumins, blood serum IT RL: BIOL (Biological study) (histamine binding by, in allergy) 51-45-6, biological studies IT RL: BIOL (Biological study) (albumins of blood serum binding of, in allergy) L32 ANSWER 14 OF 14 HCAPLUS COPYRIGHT 2003 ACS on STN 1968:75101 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: 68:75101 Specificity effects of cation binding to the macroion TITLE: in the bovine serum albumin-histamine interaction Botre, Claudio; Marchetti, Marcello; Borghi, Saverio AUTHOR(S): CORPORATE SOURCE: Univ. Rome, Rome, Italy Biochimica et Biophysica Acta (1968), 154(2), 360-6 SOURCE: CODEN: BBACAQ; ISSN: 0006-3002 DOCUMENT TYPE: Journal English LANGUAGE: The specific interaction between bovine serum albumin and histamine and the influence of the ionic medium on this interaction were studied. This interaction is dependent on ionic strength. Evidence is given for a crit. saline concn. which can be regarded as a threshold defining 2 sharply different behaviors of bovine serum albumin in the presence of histamine. Potentiometric measurements carried out by means of coupled perm-selective membrane electrodes provided data which showed that for a given ionic strength, bovine serum albumin requires an amt. of histamine which varies with the nature of the cations. Alkali binding to the bovine serum albumin macroion in the presence of histamine does not follow the sequence expected for polycarboxylic acids, since K+ proved to be the most tightly bound. 20 references. 2 (General Biochemistry) CC BINDING: HISTAMINE BINDING PROTEINS; ELECTROLYTES ALBUMINS HISTAMINE; CATIONS ALBUMINS HISTAMINE BINDING; ALBUMINS HISTAMINE BINDING; PROTEINS HISTAMINE BINDING Cations, biological studies IT (in histamine reaction with albumins) Albumins, blood serum IT RL: RCT (Reactant); RACT (Reactant or reagent) (reaction of, with histamine, cation binding effect on) 51-45-6, reactions IT RL: RCT (Reactant): RACT (Reactant or reagent) (with albumin, cation binding effect on)

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SIDSI/gcgdata/geneseq/geneseqp-embl/AA1090.DAT:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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                                                                                                                                                                                                                                      Length
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AAB74288
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                                                                                                                                                                                                                                                                                                       SUMMARIES
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                   Histacalin protein
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| tation paper amino                    | Č        | ļ        | 4     |      | :     |  |
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| A HERE                                | 2 2      | <b>၁</b> | 360   |      |       |  |
| phila melar                           | 084      | 22       | 618   |      |       |  |
| cent                                  | AAB73087 | 22       | 537   | 8.4  | •     |  |
| Human secreted pro                    | AAY86302 | 21       | 515   | 8.4  | •     |  |
| Human quiescent ce                    | ABB08992 | 23       | 492   | 8.4  | •     |  |
| Human albumin fusi                    | ABG64483 | 23       | 492   | 8.4  | 79.5  |  |
| Human albumin fusi                    | ABG64482 | 23       | 492   | 8.4  | •     |  |
| ž                                     | AAB60300 | 22       | 492   |      | 79.5  |  |
| Human gene 6 encod                    | AAE04261 | 22       | 492   | ٠.   | 79.5  |  |
| gene                                  | AAE04222 | 22       | . 492 |      |       |  |
| Human gene 88-enco                    | AAY86571 | 21       | 490   | 8.4  | 79.5  |  |
| Human secreted pro                    | AAY86332 | 21       | 490   |      |       |  |
| Human peptidase, H                    | AAY90286 | 21       | 327   |      |       |  |
| S. typhimurium env                    | AAW18384 | 18       | 246   |      | 80    |  |
| EnvF gene product.                    | AAR70739 | 16       | 246   |      | 80    |  |
| E. coli growth and                    | AAG98884 | 22       | 865   |      | Ö     |  |
| Listeria monocytog                    | ABB50006 | 23       | 246   |      | 80.5  |  |
| Streptococcus pneu                    | AAW69165 | 19       | 1965  |      | 81    |  |
| Candida albicans e                    | ABP74018 | 23       | 754   |      | 81    |  |
| Senna alpha-galact                    | AAW26604 | 18       | 406   |      | 81    |  |
| Lactococcus lactis                    | ABB54832 | 23       | 475   |      | 82.5  |  |
| ly ac                                 | ABB92332 | 23       | 850   | 8.9  | 84.5  |  |
| ı pr                                  | AAW99801 | 20       | 469   | ٠    | 84.5  |  |
| CH .                                  | ABB58634 | 22       | 277   |      | 93.5  |  |
|                                       | AAY18088 | 20       | 284   | 0    | 96    |  |
|                                       | AAY18087 | 20       | 285   | ۲    | 110   |  |
| Histamine binding                     | AAY18084 | 20       | 198   | 8    | 174   |  |
| Histamine binding                     | AAY18086 | 20       | 203   | ۲    | 207   |  |
| Histamine binding                     | AAY18085 | 20       | 203   |      | 209.5 |  |
| Histamine binding                     | AAY18081 | 20       | 209   | 5    | [43   |  |
| Tick vasoactive am                    | 44       | 19       | 209   | 5    | 4.1   |  |
| Histamine binding                     | 808      | 20       | 200   | 8    | 67.   |  |
| k vasoactive                          | 74       | 19       | 200   | 28.1 | 267.5 |  |
| Histacalin protein                    | AAB73262 | 22       | 182   | 8    | 67.   |  |
|                                       |          |          |       |      |       |  |

## ALIGNMENTS

## RESULT 1 AAB74288 ID AAB7 Nuttall PA, Paesen GC, 01-SEP-1999; 24-AUG-2000; 2000WO-GB03282 08-MAR-2001. WO200115719-A2 Unidentified Histacalin; FS-HBP1; conjunctivitis Histacalin protein FS-HBP1 20-JUN-2001 AAB74288; AAB74288 standard; (EVOL-) EVOLUTEC LTD. 2001-257675/26 (first entry) 99GB-0020674. protein; 172 ₿

Use of histacalin proteins for treating or preventing non-infective conjunctivitis, or for manufacturing a medicament for treating or preventing conjunctivitis, e.g. seasonal or perennial allergic conjunctivitis

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RESULT 2
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Best Local :
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                 allergic rhinitis. The method involves employing a blood reading cectoparasite derived (e.g. tick-derived) histacalin protein. The sequence is one such histacalin protein. The histacalin protein, useful for treating or preventing allergic rhinitis, both season perennial allergic conjunctivitis.
                                                                                                                    Use of histacalin proteins for treating or preventing allergic rhinitis, or for manufacturing a medicament for treating or preventing allergic rhinitis, e.g. seasonal or perennial allergic rhinitis -
                                                                                                                                                                       WPI;
                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                   08-MAR-2001
                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                FS-HBP1; histacalin
                                                                                                                                                                                                                                                                                                                                                                                      Histacalin
                                                                                                                                                                                             Nuttall
                                                                                                                                                                                                                  (EVOL-)
                                                                                                                                                                                                                                        01-SEP-1999;
                                                                                                                                                                                                                                                            24-AUG-2000;
                                                                                                                                                                                                                                                                                                         WO200116164-A2
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in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e present invention relates to the use of a histacalin protein r treating or preventing conjunctivitis. The present sequence the histacalin protein FS-HBP1. The invention is particularly the treatment of allergic or seasonal conjunctivitis.
                                                                             present invention relates
                                                                                                                                                                      2001-218521/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVYTSDCLPE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNVEAWFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTEDGQVLTDVLAFSDDNCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNVEAMFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTEDGQVLTDVLAFSDDNCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKPVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVYTSDCLPE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172
                                                                                                    Pages
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                                                                                                                                                                                           Paesen
                                                                                                                                                                                                                                                             2000WO-GB03287
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                    lin protein; antiinflammatory;
allergic rhinitis.
                                                                                                    4-6;
                                                                                                                                                                                                                                                                                                                                                                                      FS-HBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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                                                                                                  19pp; English.
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                                                              to a method for treating or preven involves employing a blood-feeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 952; DB 22;
Pred. No. 3.9e-94;
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                                                                                                                                                                                                                                                                                                                                                             antiallergic;
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Best Query

Local Similarity

100

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Score Pred.

952; No. 3

DB 22; .9e-94;

Length 172;

Match

Sequence

172

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RESULT 3
AAW37446
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                                                                                                                                                                                  This protein comprises tick Rhipicephalus appendiculatus (Ra) novel female-specific histamine binding protein 1 (FS-HBP1). Its amino acid sequence was deduced from a cDNA clone (see AAV00227) obtained from a salivary gland cDNA library. FS-HSP2 and male-specific HSP1 (see AAW37447-48) and a related protein, D.RET6 (see AAW37449) from Dermacenter reticularis, were also identified. These novel vasoactive amine binding proteins (VABP8) can be expressed in host cells using e.g. a baculovirus expression system. They can be used: (i) to assay histamine (or other VA such as serotonin) in the contraction of the contractio
                                                                  body fluids or cell culture supernatants, e.g. to monitor the effect of allergens; (ii) for binding VA, e.g. to remove histamine from blood, food, cell cultures etc.; (iii) as an antihistamine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Peptide
                                     anti-inflammatory agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assaying or removing histamine and anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vasoactive amine binding proteins and related nucleic acid, vectors - transformed cells and transgenic animals, used for assaying or removing histamine and as antihistamine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Female-specific vasoactive amine binding protein 1; FS-HCP1; histamine; serotonin; assay; antihistamine; anti-inflammatory; insect bite; snake bite; scorpion bite; dermatitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Fig 1; 44pp; English.
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18-MAY-1996;
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studying
                 This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and altergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rininitis; food dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine respiratory disease; coronary heart disease; cellular growth regulator tissue repair; blood-sucking ectoparasite; therapy.
                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                Histamine and serotonin binding
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Query Match Best Local S Matches 113

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                                                                                                        Use of histacalin proteins for treating or preventing conjunctivitis, or for manufacturing a medicament for preventing conjunctivitis, e.g. seasonal or perennial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rhinitis (hay fever), atopic dermatitis, insect bites and food and drualiergies, abnormal blood pressure, migraine, psychological disorders respiratory disease, and coronary heart disease). Histamine may also lused to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking
                                                                                                                                                                                                                                                                                                                  Unidentified.
                                                                           Claim 4;
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                 e present invention relates to the use of a histacalin protein reating or preventing conjunctivitis. The present sequence the histacalin protein FS-HBP1. The invention is particularly the treatment of allergic or seasonal conjunctivitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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Best Local S
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a method for treating or preventing allergic rhinitis. The method involves employing a blood-feeding ectoparasite-derived (e.g. tick-derived) histacalin protein. The presequence is one such histacalin protein. The histacalin protein, is useful for treating or preventing allergic rhinitis, both seasonal and protein of the presequence is the seasonal and the protein of the presenting allergic rhinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of histacalin proteins for treating or preventing allergic rhinitis, or for manufacturing a medicament for treating or preventing allergic rhinitis, e.g. seasonal or perennial allergic rhinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FS-HBP2; histacalin protein; antiinflammatory; antiallergic; opthalmological; allergic rhinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histacalin protein FS-HBP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB73261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Pages 4-6; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-2000; 2000WO-GB03287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              perennial allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EVOL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-218521/22
                                   121 VIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVYTSDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVOLUTEC LTD
                                                                                                                                          KNVEAWFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTEDGQVLTDVLAFSDDNCY
                                                                                                                                                                                                                                                          DKPVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDE
VIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACL
                                                                                                            KSIQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCD
                                                                                                                                                                                                                         NOPDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 AA;
                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                    66.2%;
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                                                                                                                                                                                                                                                                                                                                    Score 630; DB 22;
Pred. No. 1.7e-59;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                           Length 171;
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170
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DKPVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDE

Query Match
Best Local Similarity
Matches 113; Conserv

Conservative

20;

Score 630; pB 1 Pred. No. 2e-59; 90; Mismatches

рв 19; 37;

Length Indels

0;

Gaps

60 0

66.2%;

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RESULT 7
AAW37447
                           This protein comprises tick Rhipicephalus appendiculatus (Ra) novel CC female-specific histamine binding protein 2 (FS-HBP2). Its amino acid sequence was deduced from a cDNA clone (see AAW0728) obtained CC from a salivary gland cDNA library. FS-HSP1 (see AAW37446) and male-specific HSP1 (see AAW37448) and a related protein, D.RE76 (see CC AAW37449) from Dermacenter reticularis, were also identified. These convel vasoactive amine binding proteins (VABPs) can be expressed in bost cells using e.g. a baculovirus expression system. They can be used; (i) to assay histamine (or other VA such as serotonin) in be used; (i) to assay histamine (or other VA such as serotonin) in comparation or cell culture supernatants, e.g. to monitor the body fluids or cell cultures stor; (iii) as an antihistamine or ceffect of allergens; (ii) for binding VA, e.g. to remove histamine constructions blood, food, cell cultures etc.; (iii) as an antihistamine or anti-inflammatory agents, e.g. for treating insect, snake or scorpion bites or dermatitis, or as a carrier for slow release of histamine-related compounds; (iv) in vaccines to protect against metazoan parasites, especially in animals; (v) as reagents for the immune response etc. VABPs provide a more sensitive assay for histamine than low-affinity antibodies currently used. They may calso be more effective and safer than conventional antihistamines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      assaying or removing histamine and as antihistamine or anti-inflammatory agents
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-018506/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-1997;
18-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 2; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vasoactive amine binding proteins and related nucleic acid vectors - transformed cells and transgenic animals, used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insect bite; snake bite; scorpion bite; dermatitis;
transgenic animal; tick.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Female - specific vasoactive amine binding protein 1; FS - HCP1;
histamine; serotonin; assay; antihistamine; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tick vasoactive amine binding protein 2 FS-HBP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paesen GC;
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96GB-0010484.
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RESULT 8
AAY18079
ID AAY18079
ID AAY18079
AAY 1807
AAY 18
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                                                                             Query Match
Best Local S
Matches 113
                                                                                                                                                                                                                                                          This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various dibleases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; droormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 2; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of allergies
                                                                                                                                                                                          Sequence
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26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Histamine and serotonin binding
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                                                                                113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXFORD
                                                                                                            Similarity
DKPVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDE
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                                                                                                                                                                                          190
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paesen
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97GB-0025046.
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                                                                                                         66.2%;
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                                                                                                    Score 630; DB 20
Pred. No. 2e-59;
                                                                                Mismatches
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                                                                                                                               DB 20;
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                                                                                Indels
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                                                                                0;
                                                                             Gaps
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RESULT 10
AAB73262
ID AAB73
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AAB74290
ID AAB7
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Matches 70
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                 The present invention relates to the use of a histacalin protein for treating or preventing communctivitis. The present sequence is the histacalin protein FS-HBPI. The invention is particularly in the treatment of allergic or seasonal conjunctivitis.
                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                     Use of histacalin proteins for treating or preventing conjunctivitis, or for manufacturing a medicament for preventing conjunctivitis, e.g. seasonal or perennial
                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Histacalin; MS-HBPl; conjunctivitis
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                                                                                                                                                                                                                                                                                                                               conjunctivitis
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                                                             120 YVIYALGPDGSGAG-YELWAT-DYTDVPASCLEKFNEYAA---GLPVRDVYT-SDCLP 171
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                                                                                                                                                                                                                                                                                                          4; Page 5-6;
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                                                                                                                    63 VEAWFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTED--GQVLTDVLAFSD-DNC 119
                                                                                                                                                     3 PVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKN
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                                                                                               LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNC
                                                                                                                                          PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNVEAWFMEMNNADTVYQHTFEKATPDKMYGYNKENAITYQTEDGQVLTDVLAFSDDNCY 120
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                                                                                                                                                                                                                                                                                                          English.
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                                                                                                                                                                                              Score 267.5;
Pred. No. 1.
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                                                                                                                                                                                      Mismatches
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r treating or
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AAB73262 standard;

protein; 182

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AAW37448
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Best Local
           Male-specific vasoactive amine binding protein 1; MS-HCP1; histamine; serotonin; assay; antihistamine; anti-inflammatory; insect bite; snake bite; scorpion bite; dermatitis; vaccine; transgenic animal; tick.
                                                                                                            08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for treating or preventing allergic rhinitis. The method involves employing a blood-feeding ectoparasite-derived (e.g. tick-derived) histacalin protein. The presensequence is one such histacalin protein. The histacalin protein, is useful for treating or preventing allergic rhinitis, both seasonal and perennial allergic conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of histacalin proteins for treating or preventing allergic rhinitis, or for manufacturing a medicament for treating or preventing allergic rhinitis, e.g. seasonal or perennial allergic rhinitis
                                                                             Tick vasoactive amine binding protein 1 MS-HBP1
                                                                                                                                     AAW37448;
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                                                                                                                                                                AAW37448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opthalmological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Histacalin protein MS-HBP1
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                                                                                                                                                                                                                                               120 YVIYALGPDGSGAG-YELWAT-DYTDVPASCLEKFNEYAA---GLPVRDVYT-SDCLP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-218521/22
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                                                                                                                                                                standard;
                                                                                                                                                                                                                                 DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSCKP 177
                                                                                                                                                                                                                                                                                    LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNC
                                                                                                                                                                                                                                                                                                               VEAWFMMNNADTVYQHTFEKATPDKMYGYNKENAITYQTED--GQVLTDVLAFSD-DNC 119
                                                                                                                                                                                                                                                                                                                                         PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK 59
                                                                                                                                                                                                                                                                                                                                                                   PVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                    182
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                                                                                                                                                               Protein;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 267.5; DB 22;
Pred. No. 1.9e-20;
20; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                        182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metazoan parasites, especially in animals; (v) as reagents for studying inflammation, involvement of VA in ulcer formation or immune response etc. VABPS provide a more sensitive assay for histamine than low-affinity antibodies currently used. They may be a sensitive as a sens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vectors - transformed cells and transgenic animals, assaying or removing histamine and as antihistamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New vasoactive amine binding proteins and related nucleic vectors - transformed cells and transgenic animals, used f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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18-MAY-1996;
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138
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                                                                                                                                                                                                               63 VEAWFMEMNNADTVYQHTFEKATPDKMYGYNKENAITYQTED--GQVLTDVLAFSD-DNC 119
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DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSCKP
                                                                YVIYALGPDGSGAG-YELWAT-DYTDVPASCLEKFNEYAA---GLPVRDVYT-SDCLP
                                                                                                                                                                                                                                                                                                                                                              PVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKN 62
                                                                                                                                               LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNC 137
                                                                                                                                                                                                                                                                                          PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 AA;
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96GB-0010484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 200;
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RESULT 12 AAY18080

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                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                              This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticarial asthma, allergic rhinitis (hay fever), acopic dermatitis, insect bices and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease) Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking ectoparasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Histamine and serotonin binding compounds useful for of allergies
                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuttall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-1998;
26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhipicephalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Histamine binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Histamine binding protein MS-HBP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1999
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                                                                                                                                                                                                   Local
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DB; AAX76966.
    138
                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Fig 3; 84pp; English.
                                                                                           63
                                                               78
                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PΛ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OXFORD VACS LTD.
                                                                                                                                                                                                   Similarity
                                                                             VEAWFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTED--GQVLTDVLAFSD-DNC 119
DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSCKP
                                                                                                                                                      PVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
                                 YVIYALGPDGSGAG-YELWAT-DYTDVPASCLEKFNEYAA---GLPVRDVYT-SDCLP 171
                                                               LNATILY KNKHLTDLKESHET ITVWKAYDYTTENGIKY ETQGTRTQTFEDVFVFSDYKNC
                                                                                                                         PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK
                                                                                                                                                                                                                                                200 AA;
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paesen
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97GB-0025046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                  28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serotonin binding compound;
                                                                                                                                                                                    20;
                                                                                                                                                                               Score 267.5; DB zu;
pred. No. 2.1e-20;
pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
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                                                                                                                                                                                    11;
                                                                                                                                                                                  Gaps
    195
                                                                                                                         77
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RESULT 13 AAW37449

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60 29

EKNVEAWFMFMNNADTV-YQHTFEKATPDKMYGY-NKENAITYQTEDGQVLTDVLAFSD- 116 ENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYENDTGSWGSQFKCLQVQEIERKEE DKPVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDP-VWGNDFTCVGTAAQNLNED

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Best Loc Matches Query Match

Local

Similarity

25.1%;

Score 239; DB 19; Pred. No. 2.6e-17; Mismatches

Length Indels

Conservative

24;

82;

10;

Gaps

88 59

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cultures etc.; (iii) as an antinistantine of agents, e.g. for treating insect, snake or scorpion bites or agents, e.g. for treating insect, snake or scorpion bites or dermatitis, or as a carrier for slow release of histamine-related compounds; (iv) in vaccines to protect against metazoan parasites, especially in animals; (v) as reagents for studying inflammation, involvement of VA in ulcer formation or the immune response etc. VABPs provide a more sensitive assay for histamine than low-affinity antibodies currently used. They may also be more effective and safer than conventional antihistamines.
                                                                                                                                                                        This protein comprises tick Dermacenter reticularis (Dr) novel vasoactive amine binding protein (VABP) D.RF%. Its amino acid sequence was deduced from a cDNA clone (see AAV00230) obtained from a Dr salivary gland cDNA library. 3 Novel VASPs, designated from a Dr salivary gland cDNA library. 3 Novel VASPs, designated FS-HBP1, FS-HBP2 and MS-HBP1 (see AAW37446-48), of the tick Rhipicephalus appendiculatus have also been identified. The VABPs can be expressed in host cells using e.g. a baculovirus expression system. They can be used: (1) to assay histamine (or other VA such as serotonin) in body fluids or cell culture supernatants, e.g. to monitor the effect of allergens; (11) for binding VA, e.g. to remove histamine from blood, food, cell cultures etc.; (11) as an antihistamine or anti-inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New vasoactive amine binding proteins and related nucleic vectors - transformed cells and transgenic animals, used f assaying or removing histamine and as antihistamine or anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 4; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-1997;
18-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scorpion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW37449 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OXFO-) OXFORD VACS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998-018506/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tive amine binding protein; D.RET6; histamine; seroton
antihistamine; anti-inflammatory; insect bite; snake
on bite; dermatitis; vaccine; transgenic animal; tick.
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209
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96GB-0010484.
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1..28
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RESULT 14
AAX18081
ID AAX18081
AC AAX180
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                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are usseful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders,
                                                                                                                                                                                                                                                                                                                                                                               respiratory disease, and coronary heart disease). Histamine may also used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; allergic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of allergies
                                                                                                                                                                                                                                                                                                                                                    ectoparasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 4; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histamine and serotonin binding compounds useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-357841/30
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26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OXFO-)
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        60
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                                                                                         1 DKPVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDP-VWGNDFTCVGTAAQNLNED : |:|| | |:| ||:| ||:| |:| |:|
                                                                                                                                                                                61;
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EKNVEAWFMFMNNADTV-YQHTFEKATPDKMYGY-NKENAITYQTEDGQVLTDVLAFSD-
                                                           ENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYENDTGSWGSQFKCLQVQEIERKEE
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97GB-0025046.
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                                                                                                                                                                             24;
                                                                                                                                                                       Score 239; DB 20;
Pred. No. 2.6e-17;
4; Mismatches 82;
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Q

14 HQDAWKHLQKLYEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKNVEAWFMFMNNA

:::= = = :=::

Query Match Best Local : Matches

Similarity

22.0%;

Score 209.5; DB 20 Pred. No. 3.8e-14; 8; Mismatches 75;

Indels Length

7;

Gaps

73 5 DB 20;

Conservative

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RESULT 15
AAY18085
ID AAY18
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                                         CC This sequence is an example of a histamine or serotonin binding CC compound (A), of the invention. cDNA encoding this sequence was isolated from a mixed Boophilus microplus/Ixodes hexagonus cDNA expression CC library. The compounds are useful for regulating the action of histamine C1 and serotonin (in e.g. inflammation and gastric acid secretion), the C2 detection, quantification and removal of histamine or serotonin (in C1 animals, plants, cell cultures, food materials, or humans) and in the C2 treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergie repairs (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and C2 coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of coronary disease of the collection of the collecti
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Fig 7;
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26-NOV-1997;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-FEB-2000 (Rel. 41, Last annotation update)
Female-specific histamine-binding protein 2 precursor (Rhiploephalus appendiculatus (Brown ear tick),
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Parasitiformes; Ixodida; Ixodidae; Rhiploephalus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Salivary gland;
MEDLINE=99288454; PubMed=10360182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.25 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=34631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Cell 3:661-671(1999).
FUNCTION: BINDS HISTAMINE WITH A HIGH-AFFINITY. TH
OUTCOMPETE HISTAMINE RECEPTORS INDICATES THAT ITS
SUPPRESS INFLAMMATION DURING BLOOD FEEDING.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139
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                                                                                                                                                                                                                                                                                                                                       IPR002970; His_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVYTSDCLPE 190
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                                                                                                                                                                                                                                                                                                                   s_binding; 1.
His_binding; 1.
   190
                                                                                                                                                                                                                                                                       FEMALE-SPECIFIC HISTAMINE-BINDING PROTEIN 2.
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Query Match
Best Local
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Best Local Similarity
Matches 113; Conserv
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DISULFID
SEQUENCE
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-i- FUNCTION: BINDS HISTAMINE WITH A HIGH-AFFINITY. THE ABILITY TO OUTCOMPETE HISTAMINE RECEPTORS INDICATES THAT ITS FUNCTION IS 1 SUPPRESS INFLAMMATION DURING BLOOD FEEDING.
-i- SUBCELLULAR LOCATION: Secreted.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Male-specific histamine-binding salivary protein precursor (MS-HBP).
Rhipicephalus appendiculatus (Brown ear tick).
Eukaryota, Metazoa, Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HBPM_RHIAP
077422;
                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                             modified and this statement
                                                                                                                                                                                                                                                                                                                           dimensional structure."; Mol. Cell 3:661-671(1999).
                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Salivary gland;
MEDLINE=99288454; PubMed=10360182;
                                                                                                                  ProDom;
                                                                                                                                                               EMBL; U96082; AAC63108.1;
                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                              InterPro; IPR002970; His_binding. Pfam; PF02098; His_binding; 1.
                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                               "Tick histamine-binding proteins: isolation,
                                                                                                                                                                                                                                                                                                                                                              Paesen G.C., Adams P.L., Harlos
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=34631;
                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Similarity
                                                                                                                   PD152455;
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169 I
22851 MW;
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                                           POTENTIAL.

MALE-SPECIFIC HISTAMINE-BINDING
PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
 Score 267.5; DB 1; Pred. No. 1.1e-16;
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Pred. No. 1.3e-48;
0; Mismatches 37
                                Y SIMILARITY.
Y SIMILARITY.
C46A1C8C6BCAA008 CRC64;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2052 Amin
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REGIZHTON NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
FILING DATE: July 9,
                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: and WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: M111e1, Jungan APPLICANT: Mekalanos, John J.
APPLICANT: Mekalanos, John J.
APPLICANT: MACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 60/026,939
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                      APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 02110-2804
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Local Similarity 24.1%;
les 45; Conservative 25
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1302 VKEVLPE 1308
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o. 5695983
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                                                                                                                                                                                                                                                                                              Massachusetts
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225 Franklin Street
                   08/077,526
, 1993
                                                                                                           US/08/271,354
07/629,602
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US-08-565-861-9
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Patent No.
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                           NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/00
FILING DATE: 09-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/6
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 246 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: December 18 ATTORNEY/AGENT INFORMATION:
                                                                                  FILING DATE: 18-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (V. 20015/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
                                                                                                                                                                                                                          APPLICATION NUMBER: 08/2: FILING DATE: 06-JUL-1994
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 01-DEC
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les 27; Conserv
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              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 Franklin Street
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VENTION: SALMONELLA VACCINES
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617/542-8906
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                                                                                                                     UMBER: 07/629,602
18-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.4%; Score 80; DB 1; Length 246; 23.7%; Pred. No. 0.84; tive 21; Mismatches 46; Indels
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ER: 00786/220001
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                                                 00786/303001
                                                                                                                                                                                                                                                                                                                                                     Version #1.30
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PCT-US94-07658-9
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                                                                         Matches
                                                                                                          Query Match
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version SOFTWARE: #1.25 and WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/09 FILING DATE: July 9, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Miller, Samuel I.
APPLICANT: Mekalanos, John J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 ASGIISVTEDSDIVVRAEIAHNGEFVYDITITAKNTARAVMTLNKDGSIAGYEI 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 NDPVWGN----DFTCVGTAAQNLNEDEKNVEAWFMFMNNADTV------YQHTFEKAT 85
                                                                         . Similarity 27; Conserv
                                                                                                                                                                                             H: 246 amino acids amino acid
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NNGYWGGPSPVNLTIFGTITEE-QKQEALKEALFKF----DSINFSIIPERIQETIKRAN 164
                                   NDPVWGN----DFTCVGTAAQNLNEDEKNVEAWFMFMNNADTV-----YQHTFEKAT 85
                                                                                                                                                            TYPE: peptide
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23.7%; Pred. No. 0.84
ative 21; Mismatches
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                                                                      8.4%; Score 80; DB 5; Length 246; 23.7%; Pred. No. 0.34; tive 21; Mismatches 46; Indels
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                                                                                                                                                                                                                                                                                                        Sequence 518, App
Patent No. 647575
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           EARLIER APPLICATION NUMBER: 60/089,507
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,508
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,509
                                                                                                                                                                         CURRENT FILING DATE: 1999-12-14
                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/461,325A
                                                                                                                                                                                                                     APPLICANT: Ruben et al. TITLE OF INVENTION: 94 Human Secreted Proteins FILE REFERENCE: PZ029P1
                                                                                                                          EARLIER APPLICATION NUMBER: PCT/US99/13418
EARLIER FILING DATE: 1999-06-15
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SOFTWARE: PatentIn Ver
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CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: PCT/US99/13418
EARLIER FILING DATE: 1999-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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EARL I
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EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,510
EARLIER FILING DATE: 1998-06-16
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TYPE: PRT
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                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               322 DIYRLYHSCADPTGCGTGPDARAWDY----QACTE-INLTFASNNVTDMF 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VIYAL-----GPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 AFTVLA-MMDYPYPTDFLGPLPANPVKVGCDRLLSEAQRITGLRALAGLVYNASGSEHCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 REAFRQIKDLFLQGAYDTVR-----W--EFGTC----QPLS-DEKDLTQLFMFARN 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 QDAWKHLQKL-VEENYDLIKATYKNDPVWGNDF-TCVGTAAQNLNEDEKNVEAWFMFMNN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1998-06-22
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                                                                                                                                                                                                                                                                                                                               Application US/09461325A
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1998-06-1
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C;Species: Streptomyces lividans
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Apr-1998
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A;Introns: 19/3; 60/2; 106/2; 162/1; 265/3; 313/3; 364/2; 388/1; 467/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C01B12.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-512 <WIL>
A;Residues: 1-512 <WIL>
A;Cross-references: EMBL:Z92828; PIDN:CAB07337.1; GSPDB:GN00019;
A;Experimental source: clone C37A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, March 1997
A;Reference number: 219180
A;Accession: 719806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C37A5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S28179; A; Accession: S28179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Tsao, L.S.; Lin, L.L.; Chen, J.C.; Chen, J.H.; Hsu, W.H.
Blochim. Blochim
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GQPFDD 215
                                                                                                                                      -- NKDLKNLISKAHAKGMKVFF-
                                                                                                                                                                                                    NLNEDEKN-----VEAWFMEMNNADTVYQHTFEKAT-PDKMYGYNKENAITYQTED 104
                                                                                                                                                                                                                                                                         KGLTEKLDYIKGLGTTSIWMAPIFKNQPVQGTGKDASAGYHGYWITDFTQVDPHFGT---
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                                                                 GOVLTD 110
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Pred. No. 31;
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Pred. No. 15;
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A;Molecule type: DNA
A;Residues: 1-1377 <KUR>
A;Residues: 1-1377 <KUR>
A;Cross-references: GB:AL445566; PID:g14089625; PIDN:CAC13385.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p A;Reference number: A99512; MUID:21267165; PMID:11353084 A;Accession: D90538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein MYPU_2120 [imported] - Mycoplasma pulmonis (strain UAB C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
Search completed: August Job time: 15.7771 secs
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Best Local Similarity
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                                                                                                                 NEYAAGLPVRDVYTSDCLPE 172
                                                                                                                                                        EQIWVRNAQNEEAHAVFKNLLSSDNNSYKGYSLSVD--
                                                                                                                                                                                            ----AITYQTEDGQVLTDVLAFSDDNCYVIYALGPDGSGAGYELWATDYTDVPASCLEKF 152
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Pred. No. 5:
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RESULT 14
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SOFTWARE: PatentIn vers
SEQ ID NO 6
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APPLICANT: Underwood, Robert
TITLE OF INVENTION: QUIESCENT CELL DIPEPTIDYL PEPTIDASE:
FILE REFERENCE: 50420 CIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 537
TYPE: PRT
ORGANISM: Homo sapiens
                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,941
FILING DATE: 2 August 1994
                                                                                                                                                                                                               STREET: PALO ALTO
CITY: PALO ALTO
CTATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                           APPLICANT: BARR, PHILIF U
APPLICANT: KIEFER, MICHAEL C
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: DACE 4.1 GENE AND POLYPEPTIDES IN CELLS
                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                             ADDRESSEE:
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NEELEY PH.D.,
                                                                                                                                                                                                                                                                      E: COOLEY GODWARD CASTRO HUDDLESON & TATUM FIVE PALO ALTO SQUARE
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                 INFORMATION:
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                                     2 August 1994
N: 435
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25.9%; Pred. No. 3
                                                                                                       Release #1.0,
 RICHARD L.
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                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,941
FILING DATE: 2 August 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/447,64: FILING DATE: 23-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
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                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415)
TELEX: 380816 COOLEY PA
TELEX: 380816 COOLEY PA
                                                                                      NAME: NEELEY PH.D., RICHARD L. REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-
                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CATTO
                                                                                                                                                                                                                   CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
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                                TELEFAX:
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                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 FMNNADTVYQHTFEKATPDKMYGYNK----ENAITY-----QTEDGQVLTDVLA 113
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39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQQEVKRRVKRQVRSD---PQALYFNDPIWSNMWYLHCGDKNSRCRSEMNVQAAWKRGYT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSDDNCYVIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVR----DVYTSDC 169
                                                                                                                                                                                                                                                                                                                                                                                                                      CALIFORNIA
                 380816 COOLEY PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: COOLEY GODWARD CASTRO HUDDLESON & TATUM FIVE PALO ALTO SQUARE
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(415) 857-0663
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SEQ ID NO:
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23-MAY-1995
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3; Mismatches
                                                                                                                                                                                                                                                                                         Version #1
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RESULT 11
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; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-236-2
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                                     Sequence 1, Application US/09345469 Patent No. 6369210
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Matches
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Best Local :
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SEQ ID NO 518
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Monod, Michel TITLE OF INVENTION: Method of Treating Rhinitis and Sinusitis FILE REFERENCE: 81985/276823
CURRENT APPLICATION NUMBER: US/09/794,236
CURRENT FILING DATE: 2001-02-28
APPLICANT: Kapeller-Libermann, Rosana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/6
EARLIER FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: 60/6
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
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SOFTWARE: PatentIn version 3.0
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                        INFORMATION:
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                                                                                                                                               DIYRLYHSCADPTGCGTGPDARAWDY----QACTE-INLTFASNNVTDMF
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25.9%; Pred. No. 2.7;
tive 27; Mismatches
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; LENGTH: 492
; TYPE: PRT
; ORGANISM: HOMO s
US-09-345-469-1
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US-09-461-325-219
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Best Local
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LENGTH: 515
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/461,325A
CURRENT FILING DATE: 1999-12-14
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                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1998-06-22 NUMBER OF SEQ ID NOS: 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: PCT/US99/13418
EARLIER FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 94 Human Secreted Proteins
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EARLIER FILING DATE: 1998-06-16
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EARLIER APPLICATION NUMBER: 60/089,510
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                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                    Local
                                                       244 REAFRQIKDLFLQGAYDTVR-----W--EFGTC-----QPLS-DEKDLTQLFMFARN 287
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73 ADTVYQHTFEKATPDKMYGYNKENAITYQTE----DGQVLTDVLAFS----
                                                                              15 QDAWKHLQKL-VEENYDLIKATYKNDPVWGNDF-TCVGTAAQNLNEDEKNVEAWFMFMNN 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                 Score 79.5; DE Pred. No. 2.9; 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 79.5;
Pred. No. 2
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                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                 58;
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                                                                                                                                                                     Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 492;
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
                     -- DDNCY 120
                                                                                                                                 Gaps
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SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-447-642-2
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Search completed: August 1, 2003, 12:17:19 Job time : 16.1048 secs
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                                                                1:
307 GPD 309
                                                                                                 170 LPE 172
                                                                                                                                                             114 FSDDNCYVIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVR----DVYTSDC 169
                                                                                                                                                                                                                                                              256 ASANNSYCIVGIAYNAKIGGIRMLDGDVTDVVE-----AKSLGIRPNYIDIYSASW 306
                                                                                                                                                                                               196 GKNVVVTILDDGIERNHPDLAPNYDSYASYDVNGNDYDPSPRYDASNENKHGTRCAGEVA 255
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                                                                                                                                                                                                                                                                                 RESULT 3
US-08-790-912-3
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                                                                                                                                                                                                                                          Sequence 3, Application US/08790912
Patent No. 5976542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (215) 567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,939
FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT ITTLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
                                                                                                                                                                                     APPLICANT: Weiser, Jeffrey N. APPLICANT: Plaut, Andrew G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
COUNTRY:
ZIP: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 29-JAN-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11
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                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Leary, Kathryn
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1370 DRYRNNEHR-AGAELNKFVEDNAQETAKRQRDHYDYWYRILDEQGREKLYRNILVYDAYK: 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1429 ---- FGDDTTV----
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19103-2398
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SVYYMGYRMLDKDGAITYTHEMTHD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMY--GY---NKENAITY---QTEDGQVLTDVLAFSDDNCYVIYALGPDG--SGAGYELW 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDPVWGNDFTCVGTAAQNLNEDEKNVEAWFMFMNNA------DTVYQHTFEKATPD 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEAANGEHQDAWKHLQKLVEEN-----YD-----YD-----LIKATYK 37
                                   Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1861 amino acids
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SYSTEM: PC-DOS/MS-DOS
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US-08-790-912-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 831-494
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1964 amin
                                                                                                                                                                                                                                                                                                                                                Sequence 2, Apr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.5
Best Local Similarity 24.1
Matches 45; Conservative
                                                                                                                                                                                                                                                                                               atent No. 5976542
GENERAL INFORMATION:
APPLICANT: Welser, Jeffrey N.
APPLICANT: Plaut, Andrew G.
         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 567-2020
TELEFAX: (215) 567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,939
FILING DATE: 23-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND TITLE OF INVENTION: OF STREPTOCOCCUS
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                               STREET: 1601 Marke:
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Leary, Kathryn REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 29-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1177 TANKLLLHYNDHSSEKFDLKYQTDFANLP-----EYNLGNTGLLYTPNQFLYDRDSI 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1129 LLPFYN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1073 GTMLDASQIVSKKAEINPLTLPTVEPLSTSGKKD----SDFSKIAHYQANRALVYKNIEK 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1229 VKEVLPE 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 NCYVIYALGPDGSGAGYEL-WATDYTDVPASCLEKFNEYAAG------LPVRDVY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 TSDCLPE
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                                                                                                          RY: USA
19103-2398
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEHQDAWKHLQKLVEEN----YDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKNVEA
                                                                                                                                                                                                                                                                                                                                                                          Application US/08790912
                                                                                                                                               Pennsylvania
                                                                                                                                                                                 1601 Market Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1964 amino acids
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                                                                                                                                                                                     PANITCH SCHWARZE JACOBS & NADEL, P.C. 01 Market Street, 36th Floor
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29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.5%; Score 81; DB 24.1%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --KSTIVKYGNLVKENSLLYQKELLSAVMMKDDQVITDIVS-NKQ 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
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               Version #1.30
                                                                                                                                                                                                                                                             METHODS FOR TREATMENT PNEUMONIAE INFECTION
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Length 1964; Indels

50;

Gaps

65 80

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    seq
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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length: 2000000000
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952
1 DKPVWADEAANGEH
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Match
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Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    August 1, 2003, 12:15:04; Search time 13.1048 Seconds (without alignments) 555.330 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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                  US-09-131-750-29
US-08-790-912-4
US-08-790-912-3
US-08-790-912-2
US-08-790-912-2
US-08-790-912-2
US-08-65-861-9
US-09-461-325-250
US-09-461-325-250
US-09-461-325-219
US-09-461-325-219
US-09-345-469-1
US-09-345-469-1
US-09-345-462-2
US-08-284-941-2
US-08-284-941-2
US-08-285-38-2
US-09-316-503-2
US-09-316-503-2
US-09-316-325-338-2
US-08-286-338-2
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| RESULT 2 US-08-790-912-4 ; Sequence 4, Application US/08790912 ; Patent NO. 5976542 ; GENERAL INFORMATION: ; APPLICANT: Weiser, Jeffrey N. ; APPLICANT: Weiser, Jeffrey N. ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT ; TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION ; NUMBER OF SEQUENCES: 10 | 8.9%; Score 84 arity 25.3%; Pred. No onservative 29; Misma DEAANGEHQDAWKHLQKLVEENVD | RESULT 1  US-09-131-750-29  , Sequence 29, Application US/09131750A  Patent No. 6361964  GENERAL IMPORMATION:  APPLICANT: Kaiser, Chris A.  FITLE OF INVENTION: PROTEINS AND RELATED MOLECULES AND METHODS  FILE REFERENCE: 01997/502002  CURRENT APPLICATION NUMBER: US/09/131,750A  CURRENT FILING DATE: 1998-08-10  EARLIER APPLICATION NUMBER: 60/055,586  EARLIER FILING DATE: 1997-08-12  NUMBER OF SEQ ID NOS: 29  SOFTWARE: FastSEQ for Windows Version 4.0  LENGTH: 469  TYPE: PRT  GRAANISM: Homo sabiens, Mus musculus, Rattus norvegius | 28 74.5 7.8 459 3 US-08-473-446-14 Sequence 14, Appl 39 74.5 7.8 1394 US-09-213-053-6 Sequence 2, Appli 31 74.5 7.8 1394 US-09-213-053-2 Sequence 2, Appli 31 74.5 7.8 1347 1 US-08-93-785-8 Sequence 8, Appli 32 74 7.8 547 1 US-08-393-785-8 Sequence 8, Appli 34 74 7.8 547 1 US-08-393-785-8 Sequence 8, Appli 35 74 7.8 547 1 US-08-471-057-8 Sequence 36, Appli 37 73.5 7.7 881 2 US-09-347-878-36 Sequence 36, Appli 37 73.5 7.7 881 2 US-08-525-940-21 Sequence 21, Appli 39 73.5 7.7 915 2 US-08-976-838-21 Sequence 21, Appli 40 73.5 7.7 915 4 US-08-976-838-18 Sequence 21, Appli 37 7.7 182 3 US-08-976-838-19 Sequence 21, Appli 41 73.5 7.7 182 3 US-09-214-5558-7 Sequence 21, Appli 42 73 7.7 182 3 US-09-160-567-2 Sequence 2, Appli 44 73 7.7 182 4 US-09-160-567-2 Sequence 2, Appli 44 73 7.7 182 4 US-09-160-567-2 Sequence 2, Appli 44 73 7.7 2037 3 US-09-306-998-3 Sequence 3, Appli 54 US-09-306-998-3 Sequence 2, Appli 54 US-09-306-998-3 Sequence 2, Appli 54 US-09-306-998-3 Sequence 3, Appli 54 US-09-306-998-3 Sequence 3, Appli 54 US-09-306-998-3 Sequence 2, Appli 54 US-09-306-998-3 Sequence 3, Appli 54 US-09-306-998-3 |
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CORRESPONDENCE ADDRESS:

APPLICATION NUMBER: PCT/US00/13504 FILING DATE: 2000-05-18 APPLICATION NUMBER: 60/178,770 FILING DATE: 2000-01-28

APPLICATION NUMBER: 09/707,936 FILING DATE: 2000-11-08

2000-11-08

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US-10-103-196-17
                                                                                                                                                                                                                                                                                          SEQ ID NO 6
LENGTH: 969
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SCOTTI, SIMONE TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS FILE REFERENCE: SCH-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
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13 EHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKNVE-AW---FM 68 : |: |: |: | | || : | : : : | | | | : | : | : | | | : | : | : | | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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WINTERHAGER, ELK
REGIDOR, PEDRO
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                                                                                                        8.1%; Score 77.5; ilarity 21.3%; Pred. No. 14; Conservative 28; Mismatches
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Pred. No. 1
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US-09-989-545-14
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US-10-156-761-13509
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13509
LENGTH: 1806
                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09989545 Patent No. US20020164697A1
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                                                                                                                                             APPLICANT: Lehar, Sophie
APPLICANT: Manning, Stephen
APPLICANT: Manning, Stephen
APPLICANT: Coyle, Anthony J.
APPLICANT: Gutterrez-Ramos, Jose-Carlos
TITLE OF INVENTION: No. US20020164697Alel Th2-Specific Molecules and Uses Thereof
FILE REFERENCE: 5800-10B
                                                                                                     CURRENT APPLICATION NUMBER: US/09/989,545
CURRENT FILING DATE: 2001-11-20
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APPLICANT:
NUMBER OF SEQ ID NOS:
                 PRIOR APPLICATION NUMBER: 09/258,670 PRIOR FILING DATE: 1999-02-26
                                                            PRIOR APPLICATION NUMBER: 09/168,229
PRIOR FILING DATE: 1998-10-07
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CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OMURA, APPLICANT: IKEDA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 FKNQPVQGTGKDASAGYHGYWITDFTKVDPHFGT-----NKDLETLISKAHAKGMKVFF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 FMNNADTVYQHTFEKAT-PDKMYGYNKENAITYQTEDGQVLTD 110
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
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Pred. No. 34;
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-06-16
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: 94 Human Secreted Proteins FILE REFERENCE: PZ029P1
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SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: MacBeth, Kyle J.
APPLICANT: Williamson, Mark
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APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
FILING DATE: EARLIER FILING DATE: 1998-06-16
APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
FILING DATE: EARLIER FILING DATE: 1998-06-16
APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
FILING DATE: EARLIER FILING DATE: 1998-06-22
APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
FILING DATE: EARLIER FILING DATE: 1998-06-22
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Pred. No. 3.3;
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RESULT 12
US-10-103-196-17
Sequence 17, Application US/10103196
Publication No. US20030050466A1
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; ORGANISM: Homo
US-10-012-542-219
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 537
                                     GENERAL INFORMATION:
APPLICANT: N1 et al.
TITLE OF INVENTION: TM4SF Polynucleotides,
FILE REFERENCE: PT008P1
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APPLICANT: Huber, Brigitte T.
APPLICANT: Underwood, Robert
TITLE OF INVENTION: QUIESCENT CELL DIPEPTIDYL
FILE REFERENCE: 50420 CIP
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Best Local (
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Best Local Similarity
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CURRENT FILLING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: US/09/388,413
PRIOR FILING DATE: 1999-09-01
CURRENT APPLICATION NUMBER: US/10/103,196
CURRENT FILING DATE: 2002-03-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 8.4%; Score 79.5; DI Local Similarity 25.9%; Pred. No. 3.8; hes 44; Conservative 27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                               ADTVYQHTFEKATPDKMYGYNKENAITYQTE----DGQVLTDVLAFS------DDNCY 120
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Pred. No. 3
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                                                           Polypeptides,
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US-10-087-195-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.1%; Score 267.5; DB 14; Best Local Similarity 39.3%; Pred. No. 1.5e-21; Matches 70; Conservative 20; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8
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                 CURRENT APPLICATION NUMBER: US/10/012,542

CURRENT FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: 1998-06-16
                                                                                                                                                                                                                                    APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
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CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: PCT/GB00/03287
PRIOR FILING DATE: 2000-08-24
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APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Allergic Rhinitis
FILE REFERENCE: 2488-1-004
                                                                                                                                                                                                                          FILE REFERENCE: PZ029P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSCKP 177
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APPLICATION NUMBER:
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Matches
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SEQ ID NO 518
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Matches
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SEQ ID NO 250
LENGTH: 490
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PRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
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CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                LENGTH: 4
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les 44; Conserv
                                           322 DIYRLYHSCADPTGCGTGPDARAWDY----QACTE-INLTFASNNVTDMF 366
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  73
                                                                                         15 QDAWKHLOKL-VEENYDLIKATYKNDPVWGNDF-TCVGTAAQNLNEDEKNVEAWFMNN 72
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ADTVYQHTFEKATPDKMYGYNKENAITYQTE----DGQVLTDVLAFS----
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                                                                                                                                      8.4%; Score 79.5; Di
25.9%; Pred. No. 3.3;
Live 27; Mismatches
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25.9%; Pred. No. 3.3;
tive 27; Mismatches
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  -DDNCY 120
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Sequence 6, Application US/10087195
; Sequence 6, Application US/20020193306A1
; GEMERAL INFORMATION:
   APPLICANT: Nuttall, Patricia, Anne
   APPLICANT: Paesen, Guido, Christiaan
   TITLE OF INVENTION: Treatment of Allergic Rhinitis
   FILE REFERENCE: 2488-1-004
; CURRENT APPLICATION NUMBER: US/10/087,195
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: PCT/GB00/03287
; PRIOR APPLICATION NUMBER: PCT/GB00/03287
; PRIOR APPLICATION NUMBER: 920673.2
; PRIOR APPLICATION NUMBER: 9920673.2
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 172
; TYPE: PRT
; ORGANISM: FS-HBP1
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/085,572
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/GB00/03282
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 9920674.0
PRIOR FILING DATE: 1993-09-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
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                                                                                                  Query Match
Best Local Similarity
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                                                                                 Matches
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APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
FILE REFERENCE: 2488-1-003
                                                                                                                                                                                                         TYPE: PRT
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                                                                           66.2%; Score 630; DB 14; 66.5%; Pred. No. 1.4e-61; tive 20; Mismatches 37;
                                                                                                                     Length 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       equence 8, Application US/10085572 Publication No. US200201514001
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                                                                                                         SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                            FILE REFERENCE: 2488-1-003
CURRENT APPLICATION NUMBER: US/10/085,572
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/GB00/03282
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/GB00/03287 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: 9920673.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nuttall, Patricia, Anne
APPLICANT: Paesen, Guldo, Christlaan
TITLE OF INVENTION: Treatment of Allergic Rhinitis
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 9920674.0 PRIOR FILING DATE: 1999-09-01
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nuttall, Patricia, Ann
APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
FILE REFERENCE: 2488-1-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-09-01 NUMBER OF SEQ ID NOS: 8
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CURRENT FILING DATE: 2002-03-01
                                                                                                                                                     NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 2488-1-004
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TYPE: PRT
ORGANISM: FS-HBP
                                                                                        TYPE: PRT
                                                                   ORGANISM: MS-HBP 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACL 170
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Score 267.5;
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Query Match

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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/vi
2: /cgn2_6/ptodata/1/pubpaa/vi
3: /cgn2_6/ptodata/1/pubpaa/vi
4: /cgn2_6/ptodata/1/pubpaa/vi
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Match
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Gapop 10.0 , Gapext 0.5
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'Cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
'Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
'Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
'Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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US-10-087-195-6
US-10-085-572-7
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US-10-087-195-8
US-10-012-542-250
US-10-012-542-518
US-10-012-42-219
US-10-013-42-219
US-10-133-196-17
US-10-9961-403-6
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US-09-989-545-14
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1199.017 Million cell updates/sec
     Sequence 6, Appli
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| ť             | л¢                 | <u>.</u> | ۲.    | 42          | 41    | 40   | 39   | 38    | 37                 | 36                 | 35            | 34                 | ω<br>ω             | 32                 | 31             | 30                 | 29         | 28            | 27                 | 26     | 25            | 24          | 23          | 22            | 21  | 20       | 19                 | 18                | 17                | 16                |
|---------------|--------------------|----------|-------|-------------|-------|------|------|-------|--------------------|--------------------|---------------|--------------------|--------------------|--------------------|----------------|--------------------|------------|---------------|--------------------|--------|---------------|-------------|-------------|---------------|-----|----------|--------------------|-------------------|-------------------|-------------------|
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|               | 7.9                | 1.       | 7 9   | 7.9         | 7.9   | 7.9  | 7.9  | 7.9   | 7.9                | 7.9                | 7.9           | 7.9                | 7.9                | 7.9                | 7.9            | 7.9                | 7.9        | 7.9           | 7.9                | 7.9    | 7.9           | 7.9         | 7.9         | 7.9           |     |          | ٠                  | 7.9               |                   | 8.0               |
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| ţ             | л b                | n (      | <br>7 | 15          | 15    | 14   | 12   | 11    | 11                 | 11                 | 11            | H                  | 11                 | 11                 | 11             | 11                 | 11         | 11            | 11                 | 11     | 11            | 11          | H           | 10            | 10  | 10       | 10                 | 9                 | 15                | 9                 |
| 40            | US-10-016-1771-337 |          | -01.  | -167-749-33 | -017- | -042 | 375A | 643A- | US-09-978-187B-337 | US-09-978-757A-337 | -09-999-830A- | US-09-978-193A-337 | US-09-978-423A-337 | US-09-918-585A-337 | -09-978-824-33 | US-09-981-915A-337 | 9-999-833A | -09-978-564A- | US-09-978-403A-337 | 9      | -09-978-585A- | -09-978-608 | 9-978-189-3 | -09-999-832A- | 9-  | 78-697-3 | US-09-978-295A-337 | 9-7               | - 1               | US-09-728-914-4   |
| ddu 1110 anna | 337,               |          | 117   | 337         | 337,  | 51,  | 337, | 337,  | 337,               | Sequence 337, App  | 337,          | 337,               | 337,               | 337,               | 337,           | 337                | 337,       | 337,          | 337,               | е 337, | 337,          | 337,        | e 337,      | 337           | 337 | 337      | e 337,             | Sequence 51, Appl | Sequence 8129, Ap | Sequence 4, Appli |

## ALIGNMENTS

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; LENGTH: 172
; TYPE: PRT
; ORGANISM: FS-HBP1
US-10-085-572-6
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Best Local S
Matches 172
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                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/085,572
CURRENT FILLING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/GB00/03282
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nuttall, Patricia, Ann
APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
FILE REFERENCE: 2488-1-003
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 9920674.0 PRIOR FILING DATE: 1999-09-01
121 VIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVYTSDCLPE 172
                                                                   Similarity
                  VIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVYTSDCLPE 172
                                                                                                                                                                                                               100.0%; Score 952; DB 14; llarity 100.0%; Pred. No. 4.4e-97; Conservative 0; Mismatches 0;
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EMBL; 228165; CAA82007.1; -.

PIR; S37786; S37786.

SGD; SG0001648; MCD4.

GO; GO:0009277; C:cell wall (sensu Fung1); IDA.

GO; GO:0000324; C:vacuole (sensu Fung1); IDA.

GO; GO:0006506; P:GPI anchor blosynthesis; IDA.

InterPro: IPR007070; PigN.

Pfam; PF04987; PIgN: 1.

Hypothetical protein.

SEQUENCE 919 AA; 105693 MW; B8F1D0BF80792C6
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Vandenbol M., Bolle P.-A., Dion C., Portetelle D., Hilge
"DNA sequencing of a 36.2 kb fragment located between th
LAP loc1 of chromosome XI of Saccharomyces cerevisiae.";
Yeast 10:835-840(1994).
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Hypothetical 105.7 kDa protein in TPK3-PIR1 1
YKL165C OR YKL619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKQ5_YEAST
P36051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bloinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no waited and this statement is not removed. Usage by and for commercial the day of the statement is not removed. Usage by and for commercial the day of the statement is not removed.
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224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSCKP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK
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DTAGHSYRPYSAEYYDNVKYIDDQIPI-LIDKVNKFFADDKTAFIFTAD
                              DGSGAGYELWATDYTD------VPASCLEKFNEYAAGLPVRDVYTSD
                                                                                                  TVYQHTFEKATPDKMYGYNKENAITYQTED----GQVLTDVLAF---SDDNCYVIYALGP
                                                                                                                                  EDVSAVTKGWKSNPVNFDSFFNQSTHTYSFGSPDILPMFKDGASDPNKVDTW------
                                                                                                                                                      ENYDLIKATYKNDPVWGNDFTCVGTAAQNLN-------EDEKNVEAWFMFMNNAD
                                                                                                                                                                                                        Conservative
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                                                                -ELDAFVFRHLDQLFHNSTLNSTLDYEIRQDGNVFFLHLLGC
                                                                                                                                                                                                                    Score 88.5;
Pred. No. 4.
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                          B8F1D0BF80792C6A CRC64;
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een the
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RESULT 5
XDHD_BACSU
    RA AZEVECO V., BETTETO M.G., BESSIETES F., BOLOTIA A., BUTCHET S.,

RA BOTISS R., BOUTSIET L., Brans A., Brignell S.C., Bron S.,

RA BOTISS R., BOUTSIET L., Brans A., Expain M., Brignell S.C.,

RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Hoosepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Ropoport G., Rey M., Reynolds S.,

RA Rieger M., Ravolta C., Rocha E., Roche B., Rose M., Sadale Y.,

RA Rieger M., Ravolta C., Rocha E., Roche B., Rose M., Sadale Y.,

RA Sato T., Scanlan E., Schleich S., Schoeter R., Scoffone F.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassmotti A.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassmotti A.,

RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

RT The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XDHD_BAC
032144;
                                                                                                                                                                                                                                                        MEDLINE-21242727; PubMed-11344136; Schultz A.C., Nygaard P., Saxild H.H.; Schultz A.C., Nygaard P., Saxild H.H.; Schultz A.C., Nygaard P., Saxild H.H.; Princtional analysis of 14 genes that constitute the purine catabolic pathway in Bacillus subtilis and evidence for a novel regulon controlled by the PucR transcription activator."; J. Bacteriol. 183:3293-3302(2001).

J. Bacteriol. 183:3293-3302(2001).

-I- FUNCTION: Oxidizes hypoxanthine and xanthine to uric acid.
-I- CATALYTIC ACTIVITY: Xanthine + NAD(+) + H(2)O = urate + NADH.
-I- COPACTOR: Molybdopterin (By similarity).
                                             This
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28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98044033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit D).
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                                                                                                                                                               INDUCTION: Expression is very
                                                                                    SIMILARITY: BELONGS TO THE XANTHINE DEHYDROGENASE FAMILY.
                                                                                                        plus ammonia) and is induced during limiting-nitrogen (glutamate). Expression decreases when allantoin is aclimiting-nitrogen conditions.
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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F., Ogasawara N., Moszer I., Albertini A.M., Alloni
do V., Bertero M.G., Bessieres P., Bolotin A., Borch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM
                                                                                                                                                                                                                                            Purine catabolism.
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41, Last sequence update)
41, Last annotation update)
dehydrogenase subunit D (EC
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                                                                                                                                                                                                                   composed
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                                                                                                                                                                                                                     of four subunits:
                                                                                                                                                      low in excess nitrogen (glutamate during limiting-nitrogen conditions
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Bacillus
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Best L
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                                                                                                                                                                                                                                                                                                                                                                                                            Q05884;

Q1-EEB-1995 (Rel. 31, Created)

Q1-EEB-1995 (Rel. 31, Last sequence update)

Q1-EEB-1995 (Rel. 31, Last annotation update)

Q1-EEB-1995 (Rel. 31, Last annotation update)
                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
EMBL;
                      use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                      Tsao L.-S., Lin L.-L., Chen J.-C., Chen J.-H., Hsu W.-H.; Biochim. Biophys. Acta 1173:119-119(1993).
-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SubtiList; BG13989; pucD.
InterPro; IPR000674; Aldxan_dh_C.
Pfam; PF02738; Ald_xan_dh_C; 1.
Pfam; PF01315; Ald_xan_dh_C; 1.
Oxidoreductase; NAD; Molybdenum; |
SEQUENCE 745 AA; 80433 MW; C4.
                                                                                                                                                                                                                                                               MEDILINE=93144336; PubMed-8424949;
Tsao L.-S., Lin L.-L., Chen J.-C., Chen J.-H., Hsu
"Cloning and characterization of an alpha-amylase
Streptomyces lividans.";
                                                                                                                                                                                                               MEDLINE=93250042;
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PIR; 1
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modified
                                                                                                                                                                                                                                                  Biochim. Biophys.
                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1916;
                                                                                                                                                                                                                             ERRATUM
                                                                                                                                                                                                                                                                                                    MEDLINE=93144336;
                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces
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                                                                                                                                  linkages in oligosaccharides and polysaccharides.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRLI
                                                                                                                          KNOWN AS THE ALPHA-AMYLASE FAMILY.
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 x70255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTVYQHTFEKATPDKMYGYNKENAITYQTEDGQVLTDVLAFSDDNCYVIYALGPDGSGAG
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CAA49759.1;
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                                                                                                                                                                                                               PubMed=8485150;
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                                                                                                                                                                                                                                                                                                                            AND SEQUENCE OF
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Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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C4A3EC5F0094EF8D CRC64;
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                                . usage by http://www.i
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                                    SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Re
Gregor J., Davis N.W., Kirkpatrick H.A., Goo
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTRE_ECOLI P33129;
    Science
                  "The
                                                                                                                                                                                                 Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                    Raina S., Misslakas D., Baird L., Kumar S., Georgopoulos C.; "Identification and transcriptional analysis of the Escherichia colintre operon which is homologous to pap and related pilin operons."; J. Bacteriol. 175:5009-5021(1993).
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01-NOV-1997
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InterPro;
InterPro;
                                                                                                                                                                               "Systematic sequencing of the Escherichia coli genome: analysis the 2.4-4.1 min (110,917-193,643 bp) region."; Nucleic Acids Res. 22:1637-1639(1994).
                                                                                                                                                                                                                                                                             STRAIN-K12 / W3110;
MEDLINE-94261430; P
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93352405; PubMed-8102362; Raina S., Missiakas D., Baird L., Kumar S.,
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Enterobacteriaceae; Esche
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SIGNAL
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complete genome sequence nce 277:1453-1474(1997).
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SEQUENCE
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InterPro; IPR000015; Fimb_usher.
Pfam; PF00577; Usher; 1.
PROSITE; PS01151; FIMBRIAL_USHER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                      SALTY
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EMBL; D26562; -; NOT_ANNOTATED_CDS
EMBL; AE000123; AAC73250.1; -.
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SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.

SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.

CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A

FRAMESHIFT IN POSITION 481 WHICH CREATES TWO SEPARATE ORFS.

CAUTION: REF. 1 SEQUENCE WAS INCORRECT IN POSITION 861 ONWARD
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Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OUTER MEMBRANE USHER F
POTENTIAL.
S -> T (IN REF. 1).
QC -> HR (IN REF. 1).
E -> P (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 80.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F1748B551E4A5AAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                   262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport;
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                                                                                                                                                                                                                                                                                                                                           -NKENA--ITYQTEDGQVL-TDVLAFSDD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 9
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15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Arginine biosynthesis bifunctional protein argJ 2 [Includes: Glutama; N-acetyltransferase (EC 2.3.1.35) (Ornithine acetyltransferase)
(Ornithine transacetylase) (OATase); Amino-acid acetyltransferase
(EC 2.3.1.1) (N-acetylglutamate synthase) (AGS)] [Contains: Arginine biosynthesis bifunctional protein argJ2 alpha chain; Arginine biosynthesis bifunctional protein argJ2 beta chain].
ARGJ2 OR ALRA235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
CHAIN
LIPID
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-LT2 / SGSC1412 / ATCC 700720;

MEDLLNE-21.534948; PubMed-11677609;

MCCLelland M., Sanderson K.E., Spleth J., Clifton S.W.,

McClelland M., Sanderson K.E., Spleth J., Clifton S.W.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N.,

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Ni

Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                   ANASP
ARJ2_ANASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 14028:
MEDLINE=95394809; PubMed=7665482;
Gunn J.S., Alpuche-Aranda C.M., Loon
"Characterization of the Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                     110
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                                                                                                                                                                                                                                                                                                                                                                           86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                           ASGIISVTEDSDIVVRAEIAHNGEFVYDITITAKNTARAVMTLNKDGSIAGYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDPVWGN----YQHTFEKAT
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245
262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
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262 P
262 P
263 D
223 D
262 Q
29572 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Salmonella enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-ACYL DIGLYCERIDE (POTENTIAL).
D -> A (IN REF. 1).
QRKKAAGKMNEIQQTFKK -> PA (IN RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE LIPOPROTEIN ENVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Loomis W.P., Belden W.J., ella typhimurium pagC/pagD
                                                                                                                                                                                                                                   387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
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3 CRC64;
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chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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SOLUTION OF THE STANDERS OF TH
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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HAMAP; ME 01106; -; 1.

InterPro; IPR002813; ArgJ.

Pfam; PF01960; ArgJ; 1.

ProDom; PD004193; ArgJ; 1.

TIGRPAMS; TIGR00120; ArgJ; 1.

Arginine blosynthesis; Multifunctional enzyme; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21595285; PubMed-11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium anabacas."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
-I- FUNCTION: Catalyzes two activities which are involved in to cyclic version of arginine biosynthesis: the synthesis of acetlyglutamate from glutamate and acetyl-CoA, and of ornitransacetylation between acetylornithine and glutamate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acyltransferase;
CHAIN 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Cyanobacteria;
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATHWAY: Arginine biosynthesis; first step.

PATHWAY: Arginine biosynthesis; fifth step.

PATHWAY: Arginine biosynthesis; fifth step.

SUBUNIT: Heterotetramer of two alpha and two beta chains () similarity).

SUBCELLULAR LOCATION: Cytoplasmic (Probable).

MISCELLANEOUS: Some bacteria possess a monofunctional argJ-manla of catalyzing only the fifth step of the arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + L-glutamate = ornithine + N-acetyl-L-glutamate.
CATALYTIC ACTIVITY: Acetyl-CoA + L-glutamate = CoA + N-acety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of catalyzing only biosynthetic pathway. SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity)
360
                                                                                                                                                                                                                   267
                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AP003595; BAB75934.1;
                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                        Similarity
LNIGTDVA----TVWGCDLTE
                                                     YALGPDGSGAGYELWATDYTD
                                                                                                                                    VEAWFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTEDGQVLTDVLAFSDDNCYVI
                                                                                                                                                                                                             VTVDSAAN--YAQAKRVAKAIV--NSPLVKTAVYGADPNWGRVAMAIGKC---
                                                                                                                                                                                                                                                                VWADEAANGEHQDAWKHLQKLVEENYDLIK-ATYKNDPVWGNDFTCVGTAAQNLNEDEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                    179
387 /
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, AD2335.
                                                                                                                                                                                                                                                                                                                           Conservative
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179 ARGIN
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41145
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                                                                                                                                                                                                                                                                                                                                                                                                                                      WW;
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                                                                                                           ----DEVQVYPN---
                                                                                                                                                                                                                                                                                                                                                     Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEAVAGE (NONHYDROLYTIC) (BY B4A340DC3FF3013D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
ARGININE BIOSYNTHESIS BIFUNCTIONAL PROTEIN ARGJ2 BETA CHAIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARGININE BIOSYNTHESIS BIFU PROTEIN ARGJ2 ALPHA CHAIN
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376
                                                                                                                                                                                                                                                                                                                      red. No. 8.2;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                                           Length 387
                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 10
SYSC_YEAST
                                      EMBL; 24484; CAA28572.1; %
EMBL; 247814; CAA87802.1; %
EMBL; 247814; CAA87802.1; %
EMBL; 247819; CAA65216.1; %
EMBL; 274319; CAA98444.1; %
EMBL; 274319; CAA98444.1; %
EMBL; L15408; AAC37412.1; %
PIR; S50930; YSBYC.
HSSP; P34945; 1SER.
SGD; S0002430; SES1.
GG; GO:00045737; C:Cytoplasm; IDA.
GG; GO:0004828; F:serine-tRNA ligase ac:
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002317; tRNA-synt_2b.
InterPro; IPR006195; tRNA_1igase_II.
Pfam; PF02403; Seryl_tRNA_N; 1
Pfam; PF02403; Seryl_tRNA_N; 1
Pfam; PF02403; Seryl_tRNA_N; 1
                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentitles requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSC_YEAST
P07284;
              PRINTS; PR00981; TRN/TIGREAMS; TIGRO0414;
                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinform
the European Bioinformatics Institute. The
use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Folley L.S., Fox T.D.;
Submitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-serine + tRNA(Ser) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=97051598; PubMed=8896275;
Eide L.G., Sander C., Prydz H.;
"Sequencing and analysis of a 35.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87174725; PubMed=3031581; Weygand-Durasevic I., Johnson-Burke D., Soell D.; Weygand-Durasevic I., Johnson-Burke D., Soell D.; "Cloning and characterization of the gene coding for seryl-tRNA synthetase from Saccharomyces cerevisiae. Nucleic Acids Res. 15:1887-1904(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U1-APR-1988 (Rel. 07,
01-OCT-1996 (Rel. 34,
01-NOV-1997 (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288c / AB972;
Bowman S., Barrell B.G.,
Submitted (JAN-1994) to
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NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ligase) (SerRS).
SES1 OR SERS OR YDR023W OR YD9813.01
                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288c;
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                              TRNASYNTHSER.
AA_TRNA_LIGASE_II;
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the EMBL/GenBank/DDBJ
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Cownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
In Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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CHARACTERIZATION.
CHARACTERIZATION.
MEDLINE=20521747; PubMed=11067927;
Chiravuri M., Agarraberes F., Mathieu S.L., I
Chiravuri M., Agarraberes for Mathieu S.L., I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i6-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Dipeptidyl-peptidase II precursor (EC 3.4.14.2) (DPP II) (Dipeptidyl aminopeptidase II) (Quiescent cell proline dipeptidase) (Dipeptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aminoacyl-tRNA synthetase; Protein blosynthesis; Ligase; CONFLICT 224 224 L -> P (IN REF. 1). SEQUENCE 462 AA; 53309 MW; BBED6EA47E6F547B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence, purification, and cloning of an in protease, quiescent cell proline dipeptidase. J. Biol. Chem. 274:34053-34058(1999).
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CARBOHYD
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J. Immunol. 165:5695-5702(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF154502; AAF12747.1; EMBL; BC011907; AAH11907.1; EMBL; BC016961; AAH16961.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
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                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000073; A/b_hydrolase.
InterPro; IPR000379; Ser_estrs_site
Pfam; PF00561; abhydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; S28.002; -
Genew; HGNC:14892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                                                                                                Signal; Zymogen
                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligopeptides.

CATALYTIC ACTIVITY: Release of an N-terminal dipep XCC, preferentially when Xbb is Ala or Pro. Substroligopeptides, preferentially tripeptides.

SUBCUST: Homodimer (Probable).

SUBCELLULAR LOCATION: Lysosomal and intracellular SUBCELLULAR LOCATION: Lysosomal and intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: N-glycosylated.
MISCELLANEOUS: HAS F
TO CLEAVE SUBSTRATE
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                     121
 324
                                                 265
                                                                                              221
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                                                                                                                                                        Similarity
             VIYAL----GPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVY
DIYRLYHSCADPTGCGTGPDARAWDY----QACTE-INLTFASNNVTDMF
                                                                                              REAFRQIKDLFLQGAYDTVR-----W--EFGTC----QPLS-DEKDLTQLFMFARN
                                                                                                                    QDAWKHLQKL-VEENYDLIKATYKNDPVWGNDF-TCVGTAAQNLNEDEKNVEAWFMFMNN
                                                                     ADTVYOHTFEKATPDKMYGYNKENAITYQTE----DGQVLTDVLAFS------DDNCY
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                                                AFTVLA-MMDYPYPTDFLGPLPANPVKVGCDRLLSEAQRITGLRALAGLVYNASGSEHCY
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                                                                                                                                              Conservative
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SUBSTRATE MOLECULES AT ACIDIC
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DIPEPTIOYL-PETTIDASE I
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CHARGE RELAY SYSTEM (P)
CHARGE RELAY SYSTEM (P)
N-LINKED (GLCNAC...)
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Pred. No. 12;
27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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EMBL; 20.

PIR; T40186; "4.

"SEP; P42345; IFAP.

"SPBC"
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Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
Galibert F., Aves S.J., Xiang Z.; Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Hellroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Mooney R., Well S., Pearson D., Quall M.A., Rabbinowitsch E., Ruther ford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Robben J., Grymonprez B., Woodward J., Volckert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Cabel
                                                                                                                                                                                                                                                       use
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                            GeneDB_SPombe; SPBC30D10.10c;
                                                                                                                                                                                                                                   modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weisman R., Choder M.,
"The fission yeast TOR homolog, tor1+, is required for the response
starvation and other stresses via a conserved serine.";
J. Biol. Chem. 276:7027-7032(2001).
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                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21269225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphatidylinositol 3-kinase (PtdIns-3-kinase) (PI3K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [DENTIFICATION,
                                                                                                                                                                                           send
                                                                                                                                                                                                                                                                                                                    Oxidative stress.

Oxidative stress.

SIMILARITY: BELONGS TO THE PI3/PI4-KIN SIMILARITY: Contains 16 HEAT repeats.
                                                                                                                                                                                                                                                                                                                                                                                                        starvation conditions.

CATALTIC ACTIVITY: ATP + 1-phosphatidy1-1D-myo-inosito1 = ADP
1-phosphattdy1-1D-myo-inosito1 3-phosphate.

INDUCTION: By nitrogen and/or carbon starvation, cold, osmotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Phosphatidylinositol 3-kinase homolog reprogression and entry into stationary phase. Also onset of meiosis and sporulation under nitrogen ar
                                                                                                            , Z97992; Ch., Z97992; Ch., T40186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ins-3-kinase) (PI3K).
OR SPBC30D10.10C.
                                                                                                                                                                                           an
                                                                                                                                                                                       requires a license agreement (S an email to license@isb-sib.ch).
                IPR003151;
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IPR000403;
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                                                                                                                                                     CAB10805.1;
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5; PubMed=11096119;
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Best Local
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"Characterization of the geranylgeranyl Schizosaccharomyces pombe."; Mol. Microbiol. 29:1357-1367(1998).
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DOMAIN
SEQUENCE
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CWP1 OR SPAPB1A10.04C
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28-TEB-2003 (Rel. 41, Last sequence update)
28-TEB-2003 (Rel. 41, Last annotation update)
Protein farnesyltransferase alpha subunit (RAS proteins
farnesyltransferase alpha subunit) (RAS proteins
                                                                                                          Arellano M., Coll P.M., Yang W.,
                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission Eukaryota; Fungi; Ascomycota; Schiz
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                                                                                                                                  MEDLINE=98453135; PubMed=9781874;
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PF00454; PI3_PI4_kinase;
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PI3_4_KINASE_2;
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Pred. No. 78;
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Schizosaccharomycetes;
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RL Nature 415:871-880(2002).
                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ223304; CAA11246.1; -. EMBL; AL512562; CAC21477.1; -. HSSP; 004631; IFT1. GeneDB_Spombe; SPAPB1A10.04c; -. Interpro; IPR002088; PPTA. Pfam; PF01239; PPTA; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewar
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01239; PPTA; 5.
PROSITE; PS00904; PPTA; 3.
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SUBUNIT: Heterodimer of an alpha and a beta subunit.
SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE ALPHA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 5 PFTA repeats.
                                         159
103
                                                                           44
                                                                                                                       99
                                                                                                                                                           5 WADEAANG--EHQDAWKHLQKLVE--ENYD-----LIKATYKNDPVWG------
                                                                                                                                                                                                                            Similarity
                                                                             NDFTC - VGTAAQNLNEDEKNVEAWFMEMNNADTVYQHTFEKATPDKMYGYNKENAITYQT
EDGQVLTDVLAFSDDN-----
                                         NDYSQELKLTNELLEKDIYNNSAW----NHRFYVLFET----SKVVSWSLEEELNY--
                                                                                                                       WLDETAEDFQKNYQVWHHRQKILSLTKNYERELEFTKKMFEIDSKNYHVWSYRVWILQNF
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60 93 PFTA

95 128 PFTA

129 162 PFTA

164 196 PFTA

202 235 PFTA

294 AA; 34876 MW; 84
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                                                                                                                                                                                                                          8.2%;
                                                                                                                                                                                                       21;
                                                                                                                                                                                                                            Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                          PETA 2
PETA 3
PETA 4
PETA 5
                                                                                                                                                                                                                                                                                         840889770F11451E CRC64;
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-----LKDKILFAPDNQSAWNYLCGVLDKSGP

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PAC4_HUMAN STANDARD; PRT; 969 AA.
P29122; Q15099; Q15100; Q9UEG7; Q9UEJ1; Q9UEJ7; Q9UEJ9; Q9Y4G9; Q9Y4H0; Q9Y4H1;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Paired basic amino acid cleaving enzyme 4 precursor (EC (Subtilisin/kexin-like protease PACE4) (Subtilisin-like
                       Tsuji A., Hine C., Tamai Y., Yonemoto Bando M., Sakai E., Mori K., Akamatsu "Genomic organization and alternative kexin-like processing endoprotease.";
J. Blochem. 122:438-452(1997).
                                                                                     SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; PACE4E-I AND PACE4E-II).
MEDLINE-98021085; PubMed-9378725;
                                                                                                                                                                                MEDLINE-97335942; PubMed-9192737;
Mori K., Kii S., Tsuji A., Nagahama M.,
Akamatsu T., Nagamune H., Matsuda Y.;
                                                                                                                                                                                                                       TISSUE=Cerebellum;
                                                                                                                                                                                                                                                              "Identification of a Submitted (SEP-1996)
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95071480; PubMed-7980617;
Tsuji A., Higashine K., Hine C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a second human subtilisin-like protease gene the fes/fps region of chromosome 15."; DNA Cell Biol. 10:757-769(1991).
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Barr P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Hepatoma, and Kidney; MEDLINE-92075167; PubMed-1741956;
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Mammalia; Eutheria;
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Tsuji A., Higashine K., Hine C.,
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ALTERNATIVE SPLICING (ISOFORM PACE4CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                          ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification
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                                                                                                                                                                     A novel human
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                                                                                                                                                                                                                                                                                                                                                                                    dentification
                                                                                                                                          ining a hydrophobic clust ochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biophys.
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                                                                                                                                                        PACE4 isoform, PACE4E ydrophobic cluster at t
                                                                                                                                                                                                                                                                                                                                                                                  of novel cDNAs encoding human kexin-like
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Primates;
                                                                                                                                                                                                                                                               novel PACE4 isoform, PACE4E.";
to the EMBL/GenBank/DDBJ datab
                                                                                                                                                                                                                                                                                                     Kii S., Nagamune H., Nagahama M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding human kexin-like
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                                                                                                                                                                                                                                                                                                                                                                                                             Mori K., Tamai Y., Nagamune H.,
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Matsuda
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terminus.";
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CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
DISTRIBUTION IN BOTH NEUROENDOCKINE AND NON-NEUROENDOCKINE TISSUES
AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.

CATALYTIC ACTIVITY: Release of mature proteins from their
proproteins by cleavage of Arg-Xaa-Yaa-RG-|-Zaa bonds, where Xaa
can be any amino acid and Yaa is Arg or Lys.

COFACTOR: PACE4A-IS PROBABLY CALCIUM-DEPENDENT.

SUBUNIT: THE PACE4A-I PRECURSOR PROTEIN SEEMS TO EXIST IN THE
RETICULUM ENDOPLASMIC AS BOTH A MONOMER AND A DIMER-SIZED COMPLEX
WHEREAS MATURE PACE4A-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT
PROPEPTIOE CLEAVAGE AFFECTS ITS TERTIARY OR QUATERNARY STRUCTURE.

SUBCELLULAR LOCATION: PACE4A-I AND PACE4G-AII ARE SECRETED. PACE4G
AND PACE4GS ARE NOT SECRETED AND REMAIN PROBABLY IN ZYMOGEN FORM
IN ENDOPLASMIC RETICULUM. PACE4E-I AND PACE4E-II ARE RETAINED
INTRACELLULARLY PROBABLY THROUGH A MYDROPHOBIC CLUSTER IN THEIR C-
TERBUTURE DATEAR MYCHO BASEAUTH A MYDROPHOBIC CLUSTER IN THEIR C-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsuji A., Matsuda Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagahama M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moehring
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CEREBELLUM.

COMAIN: THE PROPERTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC RETICULUM. ISOFORM PACE4D LACKS THE PROPERTIDE DOMAIN.

SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                               ISOId=P29122-8; Sequence=VSP_005436, VSP_005437;
TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BRAIN,
PLACENTA, LUNG, SKELETAL MUSCLE, KIDNEY, PANCREAS, BUT AT
COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
EXPRESSED IN PLACENTA, PACE4B WAS ONLY FOUND IN THE EMBRYONIC
KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D A
EXPRESSED IN PLACENTA. PACE4E-I IS EXPRESSED IN CEREBELLUM,
PLACENTA AND PITUITARY. PACE4E-II IS AT LEAST PRESENT IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=8;
Name=PACE4A-1; Synonyms=PACE4;
IsoId=P29122-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=PACE4E-II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=PACE4B; Synonyms=PACE4.1;
IsoId=P29122-3; Sequence=VSP_005428, VSP_005429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P29122-5; Sequence=VSP_005430, VSP_005431;
Note=Probably enzymatically inactive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P29122-6; Sequence=VSP_005427, VSP_005434, VSP_005435;
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                                                                                       Match
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AB001914; BAA2162
                                                                      Similarity
                           EHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKNVE-AW---FM
 QQQEVKRRVKRQVRSD---PQALYFNDPIWSNMWYLHCGDKNSRCRSEMNVQAAWKRGYT
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Zheng M., Seidah N.G., Pintar J.E.;
"The developmental expression in the rat CNS and peripheral tissues of proteases PC5 and PACE4 mRNAs: comparison with other proprotein processing enzymes.";
Dev. Biol. 181:266-283(1997).

Dev. Biol. 181:266-283(1997).

"ITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p41413; Q62914; 01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.:
(Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5)
(Convertase PC5) (PC6) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20214819; PubMed=10749928; Xiang Y., Molloy S.S., Thomas L., Thomas G.; The PC6B cytoplasmic domain contains two acidic clusters that direct sorting to distinct trans-Golgi network/endosomal compartments."; Mol. Biol. Cell 11:1257-1273(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              candidate proprotein convertase nonendocrine cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1996) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JUSSON J., Vieau D., Hamelin J., Day R., Chretien M., Seids CDNA structure of the mouse and rat subtilisin/kexin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93342056;
                                                                                                                             CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-Yaa-ARG-1-Zaa bonds, where can be any amino acid and Yaa is Arg or Lys.
SUBCELLULAR LOCATION: PC5A IS SECRETED THROUGH THE REGULATED SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZE A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION EARLY ENDOSOMES (BY SIMILARITY).
Name-PC5B; Synonyms-Long;
IsoId-P41413-1; Sequence-Displayed.
Name-PC5A; Synonyms-Short;
IsoId-P41413-2; Sequence-VSP_005440
                                                                          Event-Alternative splicing; Named isoforms-2; Comment-Additional isoforms seem to exist;
                                                                                                                 ALTERNATIVE PRODUCTS:
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TISSUE SPECIFICITY: EXPRESSED IN THE INTESTINE, BRAIN, ADRENAL GLAND, ANTERIOR PITUITARY, THYROID, OVARIES, TESTIS AND LUNG. HIGHEST LEVELS ARE FOUND IN THE GUT, OVARIES, TESTIS AND LUNG. EXPRESSION IS HIGHER IN FEMALE THAN IN MALE REPRODUCTIVE ORGANS. DEVELOPMENTAL STAGE: FIRST DETECTED AT E9 IN HIGHLY RESTRICTED RECIONS OF THE NEURAL TUBE, IN CAUDAL MYOTOMES, AND AT THE MATERNO-EMBRYONIC JUNCTION OF THE UTERUS. AT E10, RESTRICTED EXPRESSION IS DETECTED IN THE OPTIC AND OTIC VESTICLES, THE ROOF CENTRESSION IN THE DEVELOPING NERVOUS SYSTEM HAS EXPANDED TO EXPRESSION IN THE DEVELOPING NERVOUS SYSTEM HAS EXPANDED TO EXPRESSION IN THE DEVELOPING NERVOUS SYSTEM HAS EXPANDED TO
                                        MULTIPLE REGIONS INCLUDING HIPPOCAMPUS, THALAMUS, HYPOTHALAMUS, BRAIN STEM, AND SPINAL CORD. EXPRESSION IS ALSO DETECTED IN SEVERAL PERIPHERAL ORGAN SYSTEMS, INCLUDING GUT, LUNG, ADRENAL
KYDNEY PRIMORDIA.
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DOMAIN: AC 1 AND AC 2 (CLUSTERS OF A SORTING INFORMATION. AC 1 DIRECTS TG WITH THE TGN SORTING PROTEIN PACS-1. F ACIDIC AMINO ACIDS) CONTAIN

SIMILARITY: Belongs to peptidase family SIMILARITY: Contains 1 homo B/P domain. SB.

use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti (See http://www.isb-sib.ch/announce/ There are no rest Usage by and restrictions EMBL outstation 18 a collaboration ioi ᇹ 9 way

InterPro; IRR000209; Peptidase\_S8.

Pfam; PF01483; P\_proprotein; PARTIAL.

PRINTS; PR007723; SUBTILISIN.

ProDom; PD000717; P\_domain; 1.

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SNART; SM00261; FU; 6.

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PROSITE; PS00137; SUBTILASE\_ASP; 1.

PROSITE; PS00137; SUBTILASE\_SER; 1.

PROSITE; PS00138; SUBTILASE\_SER; 1. EMBL; L14933; AAA99906.1; EMBL; U47014; AAA87888.1; PIR; B48225; B48225. HSSP; Q99405; IMPT. IPR006212; Furin\_repeat. IPR002884; P\_domain. 34 116 1877 1768 1789 1877 452 602 1753 1844 1877 1177 523 1173 214 388 388 227 383 383 3667 754 804 CHARGE RECHARGE RECHARGE RECHARGE RENTERNATED N-LINKED N-LINKED N-LINKED CELL ATTACHMENT 88 BY SIMILARITY.
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| Search completed: August<br>Job time : 14.4838 secs | 161   | 21<br>110  | Query Match<br>Best Local Similarity<br>Matches 29; Conserv   | CARBOHYD<br>VARSPLIC<br>VARSPLIC<br>SEQUENCE   |
| ed: Augus<br>4838 secs                              | - FMFMNNAI<br>:<br>GYTGKNIV\                                      | LQKLVEENS<br>::  :: <br>VKKRTKRDS  | imilarity<br>; Conse  | 1732<br>878<br>916<br>1877 AJ  |
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| 1, 2003, 12:15:48                                   | 67 -FMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTEDGQVLTDVLAFSDDN 118<br>: | 21 LQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKNVE-AW 66 ::  ::   :                          : :  : | Query Match 8.0%; Score 76.5; DB 1; Length 1877;<br>Best Local Similarity 25.7%; Pred. No. 1.1e+02;<br>Matches 29; Conservative 11; Mismatches 32; Indels 41; Gaps 6; | 1732 1732 N-LINKED (GLCNAC) (POTENTIAL). 878 915 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX |

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Result
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| A39490<br>JC5571<br>A39490<br>JC5570<br>F97255<br>H86628<br>T18238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B48238<br>B4 | B39490<br>H72455<br>JC2191                                     |
| subtilisin-like pr<br>subtilisin-like pr<br>subtilisin-like pr<br>fusion of alpha-gl<br>fructuronate reduc<br>lysophospholipase<br>probable proproted<br>conserved hypothet<br>hypothetical prote<br>cytadherence acces<br>hypothetical prote<br>branched-chain alp<br>alpha-L-fucosidase  | subtilisin-like pr<br>hypothetical prote<br>subtilisin-like pr |

## ALIGNMENTS

RESULT 1 S37786

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|--------------|---|--------------|
| C 223        | Db 169 -MYDHTFEDETQSSIELDAFVFRHLDQLFHNSTLNSTLDYEIRQDGNVFFLHLLGC 223   | A sy         |
|              |   | A sy         |
| ;P 127       | QY 75 TYYQHTFEKATPDKMYGYNKENAITYQTEDGQVLTDVLAFSDDNCYVIYALGP 127   | rote         |
| 168          | Db . 117 EDVSAVTKGWKSNPVNFDSFFNQSTHTYSFGSPDILPMFKDGASDPNKVDTW   | -glu         |
|              | <del></del>   | ase .        |
| D 74         | OV 27 ENYDLIKATYKNDPVWGNDFTCVGTAAONLNEDEKNVEAWFWEMNNAD 74   | (rr<br>hati  |
| 7;           | Matches 34; Conservative 30; Mismatches 64; Indels 41; Gaps   | Clo          |
|              | Query Match 9.3%; Score 88.5; DB 2; Length 919;   | yl t         |
|              | A;Map position: 11L   | rote<br>ush  |
| •            | A; Cross-references: SGD:S0001648; MIPS:YKL165c   | rote         |
|              | C; Genetics:  | rote         |
| eptember 199 | A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199                              | rote         |
| ï            | A;CTOSS-TeTerences: EMBL:2258//; NID:g40/482; PIDN:CAA81489.1; PID:g40/483  | se (<br>etal |
| ,            | A; Residues: 1-919 < VA3>   | rote         |
|              | A; Molecule type: DNA   | poso         |
|              | A:ACCESSION: 544303   | nrom         |
|              | A; Reference number: \$44563  | redu         |
| d LAP4 loc1  | A; Title: DNA seguencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci                               | rote         |
|              | Yeast 10, 35,40, 1994   | tein         |
|              | R:Vandenbol, M.: Bolle, P.A.: Dion, C.: Portetelle, D.: Hilger, F.  | rote         |
| 9; MIPS:YKL1 | A;Cross-references: EMBL:228165; NID:9486288; PIDN:CAA82007.1; PID:9486289; MIPS:YKL1                               | 1 1          |
|              | A; Residues: 1-919 <va2></va2>  |              |
|              | A: Molecule type: DNA   |              |
|              | A; kererence number: 53/9/6 A: Accession: 937995  |              |
|              | submitted to the Protein Sequence Database, March 1994  |              |
|              | R; Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.   |              |
| ī            | A;CTOSS-TETERENCES: EMBL:2208//; NID:340/482; PIDN:CAA81489.1; PID:340/483<br>A:Experimental source: strain S288C   | α,           |
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|              | A; Reference number: S37786   |              |
| AS1 and LAP4 | A;Description: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4                               |              |
|              | Rivancembut, m.; botte, r.; bron, c.; rotterette, b.; nityer, r. submitted to the EMBL Data Library. September 1933 |              |
|              | C; Accession: S37786; S37995; S44563  | •            |
| 199          | C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Oct-1999   |              |
|              | C;Species: Saccharomyces cerevisiae   |              |
|              | nypothetical protein rkilboc - yeast (Saccharomyces cerevisiae) N.alternate names hypothetical protein vkifig       |              |
|              | \$37786   |              |

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D.; Jones, J., Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Atthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
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                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-1237 <GLA>
A; Cross-references: GB:AL592022; PIDN:CAC96435.1;
A; Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AC1583
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AC1583
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A; Accession: AC1583
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internalin protein (LPXTG motif) homolog lin1204 [imported] - Listeria innocua
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A; Note: T4C21.260
C; Superfamily: Ar
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A; Residues: 1-648 <CHO>
A; Cross-references: EMBL: AL162295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z24479
A; Accession: T47896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein T4C21.260 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000
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                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 YVIYALGPDGSGAGYELWATDYT---DVPA 146
                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria
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                                                                                                    Similarity
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KYTYTLNVENLDGIKATPKEVIVYIDAVQGANITVKYEDESGNKLAENSILTGNVGEEYS
                                        KHLQKLVEENYDLIKATYKN-----DPVWGNDFT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAVWKDRNEETAYLTAWKRIQD------KLTSRLDPATGNEFLCF---KNNSQQFVS 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana hypothetical protein T4C21.260
                                                                               Conservative
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                                                                                                9.2%;
24.8%;
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Pred. No. 5.1;
                                                                                                Score 88;
Pred. No.
                                                                             Mismatches
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                                                                                                                                                                                                                  PID:g16413678; GSPDB:GN00178
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                                                                                                                  Length 1237
                                      -----CVGTAAQNLN 57
                                                                             Indels
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Voss, H.; We
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Fsihi, H.
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DNA Res.
A; Title:
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S75234
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A;Accession: S75234
A;Status: preliminary
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                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaneko, T.; Sato, S.; Kotani,
K.; Okumura, S.; Shimpo, S.;
A Res. 3, 109-136, 1996
Title: Sequence analysis of th
                                                                                                                                                                      112
206 DNLTYDKWQALVHALDETGVSLNLVNKHQEY----PFREMFTFD 245
                                                                                   157 PAIHQLLLIRYFIPPVPDDMHQFDN---IELPPQFEKILTDVINFCDLN---
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                                                                                                                                                                                                                                                                                                                                                                                                                             type: DNA
                                                                                                                                                                                                              22 QKLVEENYDL-----IKATYKNDPVWGNDFTCVGTAAQNLNEDEKNVEAWFMFMNNA 73
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                                                                                                                                                                      QKLYRESFNLQPGHLLVAIKDIRKKSIVSFKDY-----ADNLDK---
                                        SGAGYELW-----ATDYTDVPASCLEKFNEYAAGLPVRDVYTSD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSAKEILGYTLTEMPSNAQGEFSLEEQTVTYIYSKNPVPAKDITVQYTDEDGMELAPTET 894
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                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.; Tanaka, A.; Asamizu, Takeuchi, C.; Wada, T.;
                                                                                                                                                                                                                                                       Pred. No. 3.4;
4; Mismatches
                                                                                                                                                                                                                                                                                               Score 86.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                         50;
                                                                                                                                                                                                                                                                                               Length 368;
                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura,
                                                                                                                                                                      ----FLEIFN-
                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.; Yamada,
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y.; Miyajima,
Yamada, M.; Yas
                                                                                                                                                                      156
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probable oxidoreductase (EC 1.-.-) yurC [similarity] - Bacillus subtilis C:Species: Bacillus subtilis C:Species: Bacillus subtilis C:Species: Bacillus subtilis C:Species: O5-Dec-1997 \*sequence\_revision 05-Dec-1997 \*text\_change 09-Dec-2002 C:Accession: B70017
C:Accession: B70017
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A: Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, A.; Ature 390, 249-256, 1997
A:Ature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizci, A

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K:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prent deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dou il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Nature 413, 523-527, 2001

A;Title: Genome sequence of Yorsinia postis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AF0334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-745 <KUN>
A; Cross-references: GB:/
A; Experimental source: £
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable cytochrome c-type biogenesis protein YPO2743 [imported] - Yersinia C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: yurC
C; Superfamily: carbon-mono:
C; Keywords: oxidoreductase
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A; Residues: 1-408 < KUR>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                      DNCYVIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAG 158
                                                                                                                                                                                                                                                    LGRVGMALNNATTATQAFAHAYQLA-PDNNEVKLGYVEVLTRSNDPEDNQLATQMLR---
                                                                                                                                                                                                                                                                               F-----MNNADTVYQ---HTFEKATPDK---MYGYNKENAITYQTEDGQVLTDVLAFSD
                                                                                                                                                                                                                                                                                                              EQVAAWHQVAAQMPE----LRARVANEHADPLSMEDVARLGLGLRTSLQQDAGNVNDWM
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 Sun,
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24.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dehydrogenase
 Smith, H.O.;
                                                                                                                                                                                           -AMVGQDHTNLRAMSLLAFNAFEQG
                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
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Pred.
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No. 10;
                                                                                  31-Mar-2000 #text_change 19-Jan-2001
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                                                                                                                 Neisseria meningitidis (strain MC58
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 C.M.; Moxon,
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 E R
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                           Dougherty, Pizza, M.
                                                          X.E.;
Rappuoli,
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                                                          Eisen,
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Barrell,
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                          hypothetical protein UU441 [imported] - Ureaplasma C;Specles: Ureaplasma urealyticum C;Date: 18 Aug-2000 #sequence_revision 20-Aug-2000 C;Accession: H82891 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heines
                                                                                                   RESULT 9
H82891
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submitted to GenBank, February 2000 A; Description: The complete sequenc

sequence

ō,

urealyticum:

Alternate views

of

J.S.; Heiner, Ureaplasma

C.R.; Chen,

E.Y.; Cassell,

#text\_change urealyticum

20-Aug-2000

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probable transposon protein [imported] - Arabidopsis thallana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_chan C;Accession: H85048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete genome sequence of Neisseria meningitidis A;Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: B81171
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Nature 402, 769-777,
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                                                                                                                                                                                                                                                                        A; Gene: AT4g03860
                                                                                                                                                                                                                                                                                                         A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Sequence and analysis of
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A; Residues: 1-133 <T
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Matches
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                                                                                                                                                                                           L Similarity
42; Conserv
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42; Conserv
                                                                                                                                              DEAANGEHQ-DAWKHLQKLVEENYDLIKATY----KNDPVWGNDFTCVGTAAQ-NLNED
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EELFGF-PSGNGTKPKFERKELKDLWATSGNNVPLNSARSKSNQ 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PDIP----QLWAQKITALNYSGL-NLNQYGVASPCRTICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHIEKWQHLSREEQKILAE----
                                                                                           EKNVEAWFMFMNNADTVYOHTFEKATPDKMYGYNKENAITYOTEDGOVLTDVLAFSDDNC
                                                                                                                             DEDIETEYEPESWRMETKLLNKPDEVTVEEYIRFFEMND-FWGTRYPCYETLAQLGLLED
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es: GB:AE002422; (
ource: serogroup )
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                                                             ------VQHQFEKCHLETLMSY---PYATYKEERIEFLS-TLQLSIKKL
                                                                                                                                                                                                                                                                                                         :NC_001268;
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25.5%;
                                                                                                                                                                                                        8.8%;
25.6%;
                                                                                                                                                                                                                                                                                                                                                                                      sis of chromosome 4 of the plant Arabidopsis thaliana MUID:20083488; PMID:10617198
                            ----YELWATDYTDVPA-SCLEKFNE
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B, strain MC58
                                                                                                                                                                                         Score 83.5; D
Pred. No. 16;
Pred. Mismatches
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Pred. No. 1
                                                                                                                                                                                                                                                                                                       NID: g7267141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LRMNGGRLATAVSILSVMIEDN---
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                                                                                                                                                                                                                                                                                                         PIDN:CAB80809.1;
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RESULT 11
A60272
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A86811
beta-glucosidase (EC 3.2.1.21) [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis
C;Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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C;Keywords: glycosidase;
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A; Residues: 1-475 <STO>
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A;Molecule type: DNA
A;Residues: 1-450 <GLA>
A;Cross-references: GB:AE002140; GB:AF222894; NID:g6899420; PIDN:AAF30853.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                              A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
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   IgA-specific
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A; Accession: H82891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: UU441
                                                                                                                                                                                                                                                                                                                                                               ;Superfamily: Agrobacterium beta-glucosidase;Reywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                     Query Match
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Best Local
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                                                                                                                                                                                       326 SFNKRGVRMNADRGWEIHPQTIYEIAKRIQEDYGNI-SWFISEN-------
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                                                                                                                                                                                                                                                275 LWQSEA------EDLKRIKENKVDLLGVNYYHPSRVQEPEYSSDSLAQDWRPDKYYA
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                                                                                                                                                                                                                                                                            4 VWADEAANGEHQDAWKHLQKLVEENYDLIKATYKN-----DPVWGNDFTC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
 metalloendopeptidase (EC
                                                                                                                                                                                                                                                                                                                      8.78;
Similarity 17.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                            IDCWSWRNSY 429
                                                                                                      ASCLEKFNEY 155
                                                                                                                                 ---GMGVENEEHFKDEEGQIQDDYRIIFTTEHLFWLHKAIQEGSNCFGYHVW----
                                                                                                                                                          KMYGYNKENAITYQTEDGQVLTDV-LAFSDDNCYVIYALGPDGSGA-GYELWATDYTDVP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNGHIL 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRELKKYIDTLNKDDIVNNTINKYKFKNYIYDFISYYFDIINIFSAGNSYNDE--IRYRN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKNVEAWFMFMNNAD----TVYQHTFEKATPDKM------YGYNKENAITYQT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DETSENSHIKIWKELDWLIQNDVKIINHSYGWSP---NDFLNIGFYNFINGKEINDDKDF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVG----TAAQNLNED---
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                                                                                                                                                                                                                     -----VGTAAQNLNEDEKNVEAWFMFMNNADTVYQHTFEKATPD
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                                                                                                                                                                                                                                                                                                                        Score 82.5;
Pred. No. 11;
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Pred. No. 10;
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   3.4.24.13) -
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Streptococcus sanguis
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                                                                                                                                                                                                                                              A; Residues: 1-133 < PAR>
                                                                                                                                                                                                                                                             A; Molecule type: DNA
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A; Residues: 1-1668 <GIL>
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                                                                                                                                                             Query Match
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2000
                                                                                                                                             Similarity
               FWFRMAETLSTL-
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A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: G81933
A;Status: preliminary
A;Molecula from and assertions.
                                                                                                                                                                                                                                                             A; Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; A; Experimental source: serogroup A, strain Z2491 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Start codon: GTG
C;Superfamily: Streptococcus sanguis IgA-specific metalloendopeptidase
C;Keywords: hydrolase; metalloproteinase; tandem repeat; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: IgA protease; immunoglobulin Al
C;Speciles: Streptococcus sanguis
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993
C;Accession: A60272
R;Gilbert, J.V.; Plaut, A.G.; Wright, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Parkhill, J.; Achtman, M.; James, ; Holroyd, S.; Jagels, K.; Leather,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein NMAO876 [imported] - Neisseria meningitidis (strain Z2491
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Gilbert, J.V.; Plaut, A.G.; Wright, A.
Infect. Immun. 59, 7-17, 1991
A;Title: Analysis of the immunoglobulin A protease gene
A;Reference number: A60272; MUID:91100011; PMID:1987065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Comment: This protein is shown from the start of translation the start codon is shown in entry B60272.
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                                                                                             13 EHQDAWKHL----QKLVEENYDLIKATYKNDPVWG---NDFTCVGTAAQNLN-EDEKNVE
AWFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTEDGQVLTDVLAFS----DDNCYV 121
                                                 QHIEKWQHLSREEQKILAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KMY--GY---NKENAITY---QTEDGQVLTDVLAFSDDNCYVIYALGPDG--SGAGYELW
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                                                                                                                                               Conservative
                                                                                                                                                                8.6%;
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                                                                                                                                            Score 81.5; DI Pred. No. 2.6; L9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K.D.; Bentley, S.D.; Churcher, C.; Klee, S.; Moule, S.; Mungall, K.; Quail, M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                 ----VWGLVQNDDQEVHYEMLKLNAPDEASGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria menigitidis
                                                                                                                                                                                                                                                                                                               PIDN:CAB84156.1;
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-SLDLRMNGGRLATAVSILSVMIEDN---

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RA Adams N.D., Celniker S.E., Helt R.A., Evans C.A., Gocayne J.D., RA Adams N.D., Celniker S.E., Hilt R.A., Sabburner M., Henderson S.N., RA Adams N.D., Celniker S.E., Richards S., Asbburner M., Henderson S.N., RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Ffeiffer B.D., RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Ffeiffer B.D., RA Burtis M.F., Raybayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., RATII J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., Bartis M.F., Bence P.V., Berman B.P., Bhandari D., Bolshakov S., RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Carley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Cherry J.M., Carley S., Carlei J.H., Gu Z., Gana P., Harris M., Glasser K., A Durbin K.J., Evangelista C.C., Ferraz C., Ferrieza S., Fleischmann W., RA Glock A., Gong F., Gorrell J.H., Gu Z., Gana P., Harris M., Glasser K., A Batin D., Houston K.A., Howland T.J., Wei M.-H., Tlegwam C., Ma Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lin X., Mattel B., McIntosh T.C., McLeod M.P., McShrefi A., Ra McLitosh C., McLeod M.P., McShrefi A., Ra McLitosh C., McLeod M.P., McShrefi A., Ra Ra Harris R., Petist K.A., Nixon K., Nusskern D.R., Nelson D.L., Raid C., Stapleton M., Stupsk M.N.P., Smith T., Ra Ra McLitosh C., Stapleton M., Stupsk M.P., Smith T., Ra McLitosh R., Nelson K., Smith R., Shup B., Shu
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01-MAY-2000
01-MAR-2003
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               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AE003445; AAP46419.1; -. EMBL; AF060729; AAL28277.1; -. EMBL; AY060729; AAL28277.1; -. FlyBase; FBgn0030066; CG1085. InterPro; IPR0013754; HEM4. InterPro; IPR001309; ICE_D20. Pfam; PF02602; HEM4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
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                                                                                                                                                                                                                                                                     STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20196006; PubMed-10731132;
  PS01121;
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CASPASE_HIS;
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Last sequence up
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Best Local S
Matches 41
Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                                                        PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1
SMART; SM00408; IGC2; 2.
SMART; SM00111; KU; 10.
SMART; SM00209; TSP1; 7.
SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR003598;
Interpro; IPR003006;
Interpro; IPR002223;
Interpro; IPR002221;
Interpro; IPR002221;
                                                                                                                Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILINE-99457716; PubMed-10528409;
Mardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
"Expression of lacunin, a large multidomain extracellular matrix
"Expression of lacunin, a large multidomain extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lacunin precursor.
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                     PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 8.
PROSITE; PS50279; BPTI_KUNITZ_2; 10.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS50092; TSP1; 5.
Immunoglobulin domain; Protease inhibitor; Serine
                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02822; Antistasin; 4.
Pfam; PF00047; ig; 2.
Pfam; PF000014; Kunitz_BPTI; 10.
Pfam; PF00095; wap; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insect Biochem.
EMBL; AF078161;
HSSP; P12111; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9U8G8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9U8G8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004094; InterPro; IPR007110;
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                     Score 92.5;
Pred. No. 71;
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Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                       Score
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Match
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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952
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sp_phage:*
sp_plant:*
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sp_rvirus:*
sp_bacteriap:*
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sp_bacteria:*
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sp_vertebrate:*
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Q8wsk7 dermacentor Q9w3b3 drosophila Q9u898 manduca sex Q81cr6 plasmodium Q3xp49 clostridium Q3y765 streptococc Q91zx9 arabidopsis Q812e8 vibrio harv Q92cg8 listeria in Q33764 streptococc P73122 synechocyst Q81135 plasmodium Q9u0h2 plasmodium
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| 8 8 8<br>0 0 0               | - co   | 80.5        |            |        | 81     | 2 22     |             |            | 81.5        |        |        |           | 82         | 82         | 82          | 82          | 82          | 82.5       | 82.5   | 82.5         | 82.5   | 83     | 83.5   | w         |
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| 8 8 8 8                      |        | » «<br>л (л |            |        |        |          |             |            |             |        |        |           |            | •          | •           | •           |             | •          | •      | •            | •      | •      | •      |           |
| 511<br>601<br>932            | 387    | 1462        | 722        | 246    | 1964   | 754      | 1798        | 1377       | 512         | 391    | 388    | 133       | 3896       | 1914       | 1878        | 1854        | 1853        | 688        | 475    | 450          | 441    | 757    | 745    | 133       |
| 126<br>13                    | 16     | 12          | 5          | 16     | νţ     | 1 ω<br>7 | 16          | 16         | ഗ           | տ      | 10     | 16        | σ          | 2          | N           | N           | N           | ω          | 16     | 16           | 16     | 10     | 10     | 16        |
| Q931Y5<br>Q45821<br>Q62030   | Q8YPF9 | Q8JVL1      | Q9U0H5     | 88578Q | 059947 | Q9UVX1   | Q9KZ11      | Q98QZ8     | 062095      | Q9N6C3 | Q8H750 | Q9JVE2    | Q8I581     | 033762     | Q59986      | 033760      | 033761      | Q9UV05     | Q9CFI7 | Q9PQ49       | Q8RAP3 | Q9SR14 | Q9M105 | Q9K0D5    |
|                              |        | ٠           |            |        |        |          |             |            |             |        |        |           |            |            |             |             |             |            |        |              |        |        |        |           |
| Q931y5<br>Q45821 c<br>Q62030 | Q8ypf9 | Q8jv11      | Q9u0h5     | Q8y588 | 059947 | Q9uvx1   | Q9kz11      | Q98qz8     | 062095      |        | Q8h750 | N         |            |            |             |             | 033761      |            | Q9cfi7 | Q9pq49       | Q8rap3 | Q9sr14 | Q9m105 | Q9k0d5    |
|                              |        | feline infe | plasmodium | 1115   | (2)    | _ O      | streptomyce | mycoplasma | caenorhabd1 |        |        | neisseria | plasmodium | streptococ | streptococc | streptococc | streptococc | neurospora |        | ) ureaplasma |        |        |        | neisseria |

## ALIGNMENTS

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74C2I_260 OR AT3G60850.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AL162295; CAB82689.1; -. EMBL; BT002453; AA000813.1; -.
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                 Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
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SEQUENCE 64
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Teo J. Poh C.L., Zhang L.H.;

Tvibrio harveyi zinc metalloprotease.";

Submitted (MAY-2002) to the EMBL/GenBank/I

EMBL; AF508306; AAM34261.1; -.

InterPro; IPR001570; Peptidase_M4.

InterPro; IPR005075; Pep_M4_propep:

InterPro; IPR005075; Zn_MTpeptdse.

Pfam; PF01447; Peptidase_M4; 1.

Pfam; PF02868; Peptidase_M4; 1.

Pfam; PF03413; Pep_M4_propep; 1.

Pfam; PF03413; Pep_M4_propep; 1.

PFINTS; PR00730; THERMOLYSIN.

PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                          Baquero F., Brangeul L., Buchrleser C., Rusniok C., Amend A., Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurg Entlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gattler L., Goebel W., Gomez-Lopez N., Hain T., Hatf J., Jacks Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat (Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcel Paguez-Boland J.-A., Voss H., Wehland J., Cossart P.; "Comparative genomics of ristoria "Domina" Cossart P.;
ListiList; LIN01204;
Interpro; IPR001899;
Interpro; IPR006192;
Interpro; IPR001611;
Interpro; IPR001611;
Pfam; PF00746; Gram_po
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SEQUENCE
                                                                                                                      Vazquez-Boland J.-A., Voss H., Wel "Comparative genomics of Listeria Science 294:849-852(2001).
EMBL; AL596168; CAC96435.1; -.
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SEQUENCE 677 AA; 75120 MW;
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Q8ICR6;
Q1-MAR-2003
Q1-MAR-2003
Q1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBXP49;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein CPE0116.
                                                                                                                                        Proc. Natl. Acad. Sci. U.S.,
EMBL; AP003185; BAB79822.1;
Hypothetical protein; Comple
SEQUENCE 386 AA; 44316 M
                                                                                                                                                                                                                                                                   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamasi
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi
"Complete genome sequence of Clostridium perfringens,
flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11792842;
Shimip: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium perfringens.
Bacteria; Firmicutes; Clostridia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE 2017 AA; 244669 MW; 900CD398CDE14772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=36329;
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       49; Conservative
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R22.1; -.
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Apicomplexa;
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          33;
   Score 91; DB
Pred. No. 6.6;
33; Mismatches
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IR InterPro; IPR001899; Gram_pos_anchor.

IR InterPro; IPR006192; LPXTG.

InterPro; IPR006192; LPXTG.

InterPro; IPR006025; Zn_Mrpeptdse.

Pfam; PP00746; Gram_pos_anchor; 1.

R Pfam; PP04650; YSIRK_signal; 1.

R Pfam; PF04650; YSIRK_signal; 1.

R TIGRFAMS; TIGR01167; LPXTG_anchor; 1.

R TIGRFAMS; TIGR01167; YSIRK_Signal; 1.

PROSITE; PS50847; GRAM_POS_ANCHORING; 1.

PROSITE; PS50847; ZINC_PROTEASE; 1.

Cell Wall; Hydrolase; Peptidoglycan-anchor.
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-!- SUBCELLULAR LOCATION: ATTACHED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poulsen K., Reinholdt J., Jespersgaard C., Boye
Hauge M., Kilian M.;
"A comprehensive genetic study of streptococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus.
NCBI_TaxID=1305;
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                                                                      --GY---NKENAITY---QTEDGQVLTDVLAFSDDNCYVIYALGPDG--SGAGYELWATD 140
                                      YMGYRMLDKDGAITYTHEMTHD---
                                                                                                                                                                                                                                                                                                      DRYRNNEHR-AGAELNKFVEDNAQETAKRQRDHYDYWYRILDEQGREKLYRNILLYDAYK
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27.6%;
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Last annotation update)
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Synechocystis sp. (strain Bacteria; Cyanobacteria; Cyanobacteria; Cynobacteria; Cynobacteria)
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01-FEB-1997
01-MAR-2002
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EMBL; D90903; BAA17148.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 368 AA; 43031 MW; 6F4612A3BDDB17F3 CRC64
                                                                                                                  Gardner M.J., Hail N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
                    "Genome sequence of the h falciparum.";
Nature 419:498-511(2002).
EMBL; AE014823; AAN37027.
                                                                                                                                                                                                                                                                                                                                           MEDLINE-22255705; PubMed-12368864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum 
Eukaryota; Alveolata;
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01-MAR-2003 (TrEMBLrel. 23, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical protein, conserved.
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., N
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimu
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-97061201; Pu Kaneko T., Sato S.,
Hypothetical
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(TrEMBLrel. 02, Last sequence up)
(TrEMBLrel. 20, Last annotation protein slr1920.
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24; Mismatches
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Matches 31
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01-JAN-1998
01-MAR-2003
MEDLINE-98084472; PubMed-9423856; Poulsen K., Reinholdt J., Jespers Hauge M., Kilian M.;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
Hypothetical 229.7 kDa prot
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                                                                          Streptococcus sanguis
Bacteria; Firmicutes;
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                                                       NCBI_TaxID=1305;
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                                                                                                                                                                                                                                                                                DHVQMDKHSIAIINDNIDLINDNVGTSCDNVQFPIEKNDRVKDKFYENCDELFYENIQNV
                                                                                                                                                                                                                                                                                                   EHQDAWKHLQKLVEENYDLIKATY------KNDPVWGNDF-TCVGTAAQNLNED
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Alveolata;
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                                                                           Lactobacillales;
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          Jespersgaard
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Last sequence update)
Last annotation update
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Pred. No. 1.4e
24; Mismatches
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Pred. No.
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annotation updat
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                                                                                                                                                   InterPro; IPR005877; Gpos_YSIRK.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR006192; LPXTG.
InterPro; IPR006025; Zn_WTpeptdse.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF04650; YSIRK_signal; 1.
TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
TIGRFAMS; TIGR01168; YSIRK_signal; 1.
PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
Cell wall; Hydrolase; Peptidoglycan_anchor; 1.
Cell wall; Hydrolase; Peptidoglycan_anchor; 1.
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01-JAN-1998 (TrEMBLrel. 05, La
01-MAR-2003 (TrEMBLrel. 23, La
Igal protease (EC 3.4.24.13).
                                                                                                                                                                                                                                                                                                                                    proteases: evidence for recombination Infect. Immun. 66:181-190(1998).
-!- SUBCELLULAR LOCATION: ATTACHED TO
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PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 1237 AA; 137104 MW; FDF3655
                                                                                                                                                                                                                                                                                                 MEROPS; M26.001
                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98084472; PubMed=9423856;
Poulsen K., Reinholdt J., Jespersgaard C.,
Hauge M., Kilian M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus sanguis.
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                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                           comprehensive genetic study of streptococcal immunoglobulin
                                                                                                                                                                                                                                                                                                            AN AMIDE BOND (BY SIMILARITY).
L; Y13460; CAA73857.1; '-.
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NDPVWGNDFTCVGTAAQNLNEDEKNVEAWFMF------MNNADTVYQHTFEKATPDKMY
                                     DRYRNNEHR-AGAELNKFVEDNAQETAKRQRDHYDYWYRILDEQGREKLYRNILLYDAYK 1428
                                                               DEAANGEHQDAWKHLQKLVEEN------
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                                                                                                                                           1854 AA;
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                                                                                        Conservative
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                                                                                                 9.2%;
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                                                                                                                                          ; Peptidoglycan-anchor; Protease 205915 MW; 09AF960055C8EE30 CR
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                                                                                       Score 88; DB Pred. No. 89; 3; Mismatches
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Pred. No.
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89;
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RESULT 11
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Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF04650; YSIRK_19gnal; 1.
TIGRPAMS; TIGR01167; LPXTG_anchor; 1.
TIGRPAMS; TIGR011167; LPXTG_anchor; 1.
TIGRPAMS; TIGR011168; YSIRK_19gnal; 1.
PROSITE; PS50847; GRAM_POS_ANCHORING;
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A comprehensive genetic study of streptococcal i proteases: evidence for recombination within and Infect. Immun. 66:181-190(1998).
-i- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poulsen K., Reinholdt J., Hauge M., Kilian M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SK11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR005877; Gpos_YSIRK.
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5; Y13455; CAA7
1524 LLQAP 1528
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                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                           --GY---NKENAITY---QTEDGQVLTDVLAFSDDNCYVIYALGPDG--SGAGYELWATD 140
                                           YTDVP 145
                                                                                                                                                                                                                                NDPVWGNDFTCVGTAAQNLNEDEKNVEAWFMF------MNNADTVYQHTFEKATPDKMY
                                                                                                  YMGYRMLDKDGAITYTHEMTHD-
                                                                                                                                                                                                 ----FGDD-TTVGKATAEAQFDSSNPAMKYFFGPVGNKVVHNKHGAY---
                                                                                                                                                                                                                                                                                                 DRYRNNEHR-AGAELNKFVEDNAQETAKRQRDHYDYWYRILDEQGREKLYRNILLYDAYK
                                                                                                                                                                                                                                                                                                                                                  DEAANGEHQDAWKHLQKLVEEN-----YD--
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IPR006192; LPXTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Peptidoglycan-anchor; 1854 AA; 206031 MW; 0538AB0389
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          9.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                   13;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0538AB0389968B58 CRC64;
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RESULT P73122

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Search completed: August 1, 2003, 12:19:57 Job time: 51.4705 secs
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R InterPro; IPR006192; LPXTG.
R InterPro; IPR006192; LPXTG.
R InterPro; IPR006192; LPXTG.
R InterPro; IPR006025; Zn_MTpeptdse.
R InterPro; IPR006025; Zn_MTpeptdse.
R Pfam; PF00746; Gram_pos_anchor; 1.
R Pfam; PF00750; YSIRK_signal; 1.
R TIGREAMS; TIGR01168; YSIRK_signal; 1.
R TIGREAMS; TIGR01168; YSIRK_signal; 1.
R PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
R PROSITE; PS01042; ZINC_PROTEASE; 1.
R PROSITE; PS01042; ZINC_PROTEASE; 1.
R PROSITE; PS01042; ZINC_PROTEASE; 1.
Cell wall; Hydrolase; Peptldoglycan-anchor; Protease.
G SEQUENCE 1874 AA; 207888 MW; FA30684926BB4532 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.9%; Score 85; DB 2; Length 1874; Best Local Similarity 27.6%; Pred. No. 1.7e+02; Matches 51; Conservative 13; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A comprehensive genetic study of streptococcal immunoglobulin Al proteases: evidence for recombination within and between species."; Infect. Immun. 66:181-190(1998).
-I- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY AN AMIDE BOND (BY SIMILARITY).
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                                                                                                                                                                                                             141 YTDVP 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 NDPVWGNDFTCVGTAAQNLNEDEKNVEAWFWF------MNNADTVYQHTFEKATPDKMY 90
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Maximum DB seq
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1 NPTWANEAKLGSYQDAWKSL.....EKTVRNVYTDSSCKPAPAQN 182
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:/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep: *
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4 US-10-085-572-7

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US-09-815-242-10728

US-09-815-242-1728

US-09-95-542-9

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Compugen Ltd
Sequence 8, Appli
Sequence 7, Appli
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Sequence 10728, A
Sequence 10728, A
Sequence 172, Appli
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Sequence 273, Appli
Sequence 269, Appli
Sequence 588, App
                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                          Sequence 8, Application US/10085572

Publication No. US20020151499A1

GENERAL INFORMATION:
APPLICANT: Nuttell, Patricia, Ann
APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
FILE REFERENCE: 2488-1-003

CURRENT APPLICATION NUMBER: US/10/085,572

CURRENT FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: PCT/GB00/03282

PRIOR APPLICATION NUMBER: 9920674.0

PRIOR FILING DATE: 1999-09-01

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 182

TYPE: PRT

ORGANISM: MS-HBP 1

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Best Local Sim
Matches 182;
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                                                                      61 NATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNCD
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182; Conser
                                                                                                                                          VIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSCKPAPA
                                                                                                                                                                                                           100.0%; Score 989; DB 14; llarity 100.0%; Pred. No. 3.7e-99; Conservative 0; Mismatches 0;
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US-10-175-737-588
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US-10-176-482-588
US-10-176-482-588
US-10-176-913-588
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; LENGTH: 171
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US-10-085-572-7
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                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10085572 Publication No. US20020151499A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/10087195 Publication No. US20020193306A1 GENERAL INFORMATION:
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                                                                           SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 8
                                                                                                                               PRIOR APPLICATION NUMBER: PCT/GB00/03282
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 9920674.0
PRIOR FILING DATE: 1999-09-01
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/085,572
CURRENT FILING DATE: 2002-02-27
                                                                                                                                                                                                                                                 APPLICANT: Nuttall, Patricia, Ann
APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
FILE REFERENCE: 2488-1-003
                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 9920673.2
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/087,195
CURRENT FILING DATE: 2002-03-01
                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/GB00/03287 PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nuttall, APPLICANT: Paesen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: Nuttall, Patricia, Anne
PPLICANT: Paesen, Guido, Christiaan
TILE OF INVENTION: Treatment of Allergic Rhinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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181 QN
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Pred. No. 3.7e-99;
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; LENGTH: 171
; TYPE: PRT
; ORGANISM: FS-HBP 2
US-10-087-195-7
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US-10-085-572-6
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US-10-087-195-7
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                                                                                                                                                                                                                        Sequence 6, Application US/10085572 Publication No. US20020151499A1 GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Publication No. US20020193306A1 GENERAL INFORMATION:
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                                                         CURRENT APPLICATION NUMBER: US/10/085,572
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/GB00/03282
PRIOR FILING DATE: 2000-08-24
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                                                                                                                                           APPLICANT: Nuttall, Patricia, Ann
APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
FILE REFERENCE: 2488-1-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 2488-1-004
CURRENT APPLICATION NUMBER: US/10/087,195
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: PCT/GB00/03287
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 9920673.2
PRIOR APPLICATION NUMBER: 9920674.0 PRIOR FILING DATE: 1999-09-01 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Paesen, Guido, Christiaan TITLE OF INVENTION: Treatment of Allergic Rhinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nuttall, APPLICANT: Paesen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 IQAEFLEMNNADTNMQFATEKVTAVKMYGYNRENAFRYETED--GQVFTDVIAYSD-DNC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETED--GQVFTDVIAYSD-DNC
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Guido, Christiaan
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42.0%; Pred. No. 5.
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Pred. No. 5.3e-28;
9; Mismatches 62;
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; SEQ ID NO 6
; LENGTH: 172
; TYPE: PRT
; ORCANISM: FS-HBP1
US-10-087-195-6
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; TYPE: PRT
; ORGANISM: FS-HBP1
US-10-085-572-6
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                                                                                       Sequence 10728, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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Best Local 9
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APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Nuttall, Patricia, Anne
APPLICANT: Paesen, Guido, Christian
TITLE OF INVENTION: Treatment of Allergic Rhinitis
FILE REFERENCE: 2488-1-004
CURRENT APPLICATION NUMBER: US/10/087,195
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: PCT/GB00/03287
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
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PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                63 VEAWFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTED--GQVLTDVLAFSD-DNC 119
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; Pred. No. 4.5e-21;
20; Mismatches 77; Indels
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
                                                                 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 221
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LENGTH: 778
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APPLICANT: KANTOR, FRED S.
APPLICANT: FIKRIG, EROL
APPLICANT: DAS, SUBRATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09728914
Patent No. US20010046499A1
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TYPE: PRT ORGANISM: Ixodes scapularis-09-728-914-4
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/728,914
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 60/169,048
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/240,716
PRIOR FILING DATE: 2000-10-16
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                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TICK ANTIGENS AND COMPOSITIONS AND METHODS COMPRISING TITLE OF INVENTION: THEM FILE REFERENCE: YU-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                               NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 SKAEYEKAKATPIDEGLVPLKASDDN-RKVVD--NYVKEVINEVKAKTGKNVYTD 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 IFVPKERGS----DEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 GKHLSELDLPQTALLAGMPQAPNSYDPYT-----KPDTAKER-----RDVVLYTMYDNKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 QEAWMAVRLEREKSKEEILTYYI-NKVYMANGFYGME----TAAEN-----YY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 NKHLTDLKESHETITVW-----KAYD-YTTENGIKYETQGTRTQTFEDVFVFSDYKNCDV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 QDAWKSLQQDQNK-----RYYLAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNATILYK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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Yamamoto, Robert T.
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; Pred. No. 3.1;
25; Mismatches
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RESULT 10
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; LOCATION: (115)
; OTHER INFORMATION: amino acid at this position is unknown
US-09-995-542-9
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                                                                  Sequence 172, Application US/09893737 Patent No. US20020110855A1 GENERAL INFORMATION:
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Best Local :
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         APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/995,542
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/253,520
PRIOR FILING DATE: 2000-11-28
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Patent No. US20020127647A1
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SOFTWARE: PatentIn Ver
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TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                               349 FHDLEGMWEELSPQIWTFMENSQEMDLVRTLLDSRGND----QFW--EQKLDGLDWTAQD 402
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                                                                                                                                                                                                                                                                                                                                                                 61 NATILYKNKHLTDLKESHETITVWKAYDYTTENGIKY--ETQGTR-----TQTFEDVFV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 DYTDFSGNPVQCENFRVMEKRTPTNYSFQYRYKSKNSWETIDETLILKDIGEHGFPNVMN 144
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                            IMAFLAKNPEDVQSPNGSVYT 423
                                                                                                                                                                                                                            TMAYFAQQQEKTVR---NVYT 171
                                                                                                                                                                                                                                                                                                  FSDYKNCDVIFVPK------
                                                                                                                                                                                                                                                                                                                                  NSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAV
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Pred. No. 85;
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79; DB 9; Length 221; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                  ---ERGSDEGDYELWVSEDKIDKIPDCCKF 153
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RESULT 11
US-09-864-761-48672
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US-09-893-737-172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48672, Application Patent No. US20020048763A1
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Best Local Similarity
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CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
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                                        FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03
                                                                                                                             APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 24263.6
                    APPLICATION NUMBER: PCT/US01/00661
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Hanzel, Wensheng
                                                                                                        CATION NUMBER: PCT/US01/00663
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Hanzel, David K.
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Pred. No. 2
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RESULT 13
US-09-731-872-269
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                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-231-2
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PATENT NO. US20010049434A1
GENERAL INFORMATION:
APPLICANT: CONKLIN, Darrell C.
TITLE OF INVENTION: Human Ribonuclease
FILE REFERENCE: 00-19
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/801,231
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 199
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NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 48672

LENGTH: 198
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Best Local
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Best Local :
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EST_HUMAN HIT: AW188146.1, EVALUE 1.00e
OTHER INFORMATION: SWISSPROT HIT: P00673, EVALUE 1.00e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/774,203
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Similarity 20.8%;
33; Conservative 2
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                                                                                                                                                                               ITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSDE---GDYEL 137
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                                                                            W---RKVSEANGSCKWS-NNFIRSSTEVMRRVHRAPSCK 138
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                                                                                                             WVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSCK 176
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Pred. No. 4.4;
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Pred. No. 4.4;
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US-10-052-586-588
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; LOCATION: -16..-1
US-09-731-872-269
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-12
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
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SEQ ID NO 269
LENGTH: 199
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Publication No.
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                   APPLICANT: Zhang, Zemin TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C1 CURRENT APPLICATION NUMBER: US/10/052,586 CURRENT FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
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APPLICANT: Bougueleret, Lydde
APPLICANT: Bougueleret, Eydde
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
CURRENT EPPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
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                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                            Wood, William I.
                                                                                                                                                                                                                                                                                                                                                 Watanabe, Colin K.
                                                                                                                                                                                                                                                                                                                                                                      Smith, Victoria
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b. US20020127584A1
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Pred. No. 4.4;
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OR APPLICATION NUMBER: 60/063486
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063540
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063541
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063544
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063564
OR APPLICATION NUMBER: 60/063564
OR APPLICATION NUMBER: 60/063734
OR APPLICATION NUMBER: 60/063734
OR FILING DATE: 1997-10-31
OR APPLICATION NUMBER: 60/064103
OR FILING DATE: 1997-10-31
OR APPLICATION NUMBER: 60/065311
OR APPLICATION NUMBER: 60/066120
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066466
OR FILING DATE: 1997-11-24
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Godowski, Paul J.
Gurney, Austin L.
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      GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/1aa/Packfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
      US-09-107-532A-5364
US-09-107-532A-5304
US-09-107-532A-5304
US-09-107-532A-5667
US-09-563-269-19
US-09-318-352-6764
US-09-071-035-396
US-09-071-035-398
US-09-071-035-398
US-09-071-035-398
US-09-071-035-398
US-09-18-452A-1120
US-09-634-238-269
US-09-634-238-269
US-09-634-238-269
US-09-634-238-269
US-09-634-238-269
US-09-252-991A-23258
US-09-252-991A-23258
US-09-253-991A-17272
US-09-536-784-218
US-09-253-784-80
US-09-253-784-80
US-09-253-784-80
US-09-253-784-80
US-09-253-784-80
US-09-253-784-80
US-09-253-784-786
US-09-253-784-786
US-08-290-448A-76
US-08-290-448A-76
US-08-290-448A-76
US-08-290-448A-76
US-08-290-448A-76
US-08-461-9398-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-807-022A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     555.330 Million cell updates/sec
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sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
Sequence
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                                                                                                                                                                31.5 Appli

38.5 Appli

5304 Appl

5667 Appl

24. Appl

6764 Appl

5764 Appl
                   5, Appli
5, Appli
2, Appli
76, Appl
76, Appl
76, Appl
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US-07-807-022A-1
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Result

| 5                | 44               | 43              | 42               | 41                | 40                | 39                | 3<br>8            | 37               | 36                  | 35                | 34                  | 33               | 32               | 31                | 30                 | 29               | 28                  |
|------------------|------------------|-----------------|------------------|-------------------|-------------------|-------------------|-------------------|------------------|---------------------|-------------------|---------------------|------------------|------------------|-------------------|--------------------|------------------|---------------------|
| 70               | 70               | 70              | 70               | 70                | 70                | 70                | 70                | 70               | 70                  | 70                | 70.5                | 70.5             | 71               | 71                | 71                 | 71               | 71.5                |
| 7.1              | 7.1              | 7.1             | 7.1              | 7.1               | 7.1               | 7.1               | 7.1               | 7.1              | 7.1                 | 7.1               | 7.1                 | 7.1              | 7.2              | 7.2               | 7.2                | 7.2              | 7.2                 |
| 890              | 890              | 890             | 862              | 851               | 851               | 851               | 845               | 603              | 471                 | 246               | 816                 | 240              | 972              | 972               | 648                | 620              | 805                 |
| N                | N                | ۳               | 4                | 4                 | 4                 | 4                 | 4                 | 4                | 4                   | w                 | 4                   | ω                | 4                | w                 | 4                  | 4                | 4                   |
| US-08-461-146C-8 | US-08-323-460A-8 | US-08-472-934-8 | US-09-206-551-15 | US-09-071-035-334 | US-09-071-035-330 | US-09-071-035-326 | US-08-851-567B-37 | US-09-508-264A-1 | US-09-134-001C-4125 | US-09-113-750A-34 | US-09-107-532A-3862 | US-08-824-692-23 | US-09-129-366-24 | US-08-335-844A-24 | US-09-199-637A-221 | US-08-637-670-40 | US-09-134-001C-4821 |
| Sequence 8,      | Sequence 8,      | Sequence 8,     | Sequence 15      | Sequence 33       | Sequence 330      | Sequence 326      | Sequence 37       | Sequence 1,      | Sequence 41         | Sequence 34       | Sequence 38         | Sequence 23,     | Sequence 24      | Sequence 24,      | Sequence 221       | Sequence 40,     | Sequence 48         |
| Appli            | Appl1            | Appli           | , Appl           | 334, App          | 0, App            | •                 | , Appl            | App11            | 1125, Ap            | 34, Appl          | 3862, Ap            | , Appl           | , Appl           | Appl              | 11, App            | ), Appl          | 1821, Ap            |

## ALIGNMENTS

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US-07-807-022A-1.
                  Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 908-594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07807022A
Patent No. 5321010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/807
ETILING DATE: 19911210
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PATT, Richard S.
REGISTRATION NUMBER: 32,586
REFERENCE/DOCKET NUMBER: 1814
TELECHMONE: (908) 594-4958
TELEPHONE: (908) 594-4958
TELEPHONE: 908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: F.C.
STREE
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APPLICANT: Neeper, Michael
APPLICANT: Waxman, Lloyd
TITLE OF INVENTION: Protein
TITLE OF INVENTION: Platelet
                                                                                                                                                                                                                                         STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
Local 5, 39;
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.. 8.0%;
Similarity 21.4%;
39; Conservative 30
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                                                                                                                                                                                                                                                                                                                                 unknown
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             30;
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                  Score 79.5; DB 1; Pred. No. 0.75; 0; Mismatches 86;
                                                                                                      Length 202;
                       Indels 27;
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                       Gaps
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                                                                                                                                         ; LOCATION: (B) LOCATION 1...1095; SEQUENCE DESCRIPTION: SEQ ID NO: 3855: US-09-107-532A-3855
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GENERAL INFORMATION:
                                                                       Matches
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3855:
                                                                                        ocal
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: ATINIELLO, Pamella Beneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:

LENGTH: 1095 amino acids

TYPE: amino acid

TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
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   819
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                                 15 DAWKSLQQ--DQNKRYYLAQATQT----TDGVWGEEFTCVSVTAEKIGKKKLNATI--- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33
                                                                       49;
                                                                    h 7.9%;
Similarity 23.0%;
49; Conservative
DATKAAQEKDEKAKPVVIAETSATLANKEKTGTWKIQH---KLTAEQV----LNKTIVLF 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
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                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDESQETYTKTKVYITTRLGRSGDRNHMGVSLQGYNHTGIEYKMIYDDDQGCAILKVTKD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDIWKT - - YSKSKVFWLLRRTYWVD - - - GKRSLCRYGTVLK - - RDKANHRI - - - EQIMGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7310
                                                                    ; Score 78; D3
; Pred. No. 12;
34; Mismatches
                                                                                                      D3 4;
                                                                     64;
                                                                                                      Length 1095;
                                                                    Indels
                                                                     66;
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US-09-107-532A-5304
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                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5304, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 5304: SEQUENCE CHARACTERISTICS:
                                                                 ocal
                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...468
SEQUENCE DESCRIPTION: SEQ ID NO: 5304:
                                                                                                                                                                                                                                                                                           TOPÓLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
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12 SYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNA-TILYKNKH 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
                                              32;
                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKID--KIPDCCKFTMAYFAQQQEKTVRNVYTD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LYKNKH----
                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVVDMFDDVSITHDVLDGSKEAFETILYALLPDGTNKEIWKSGKIEYEVNDKEFTKTVLA 987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASC.
                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 468 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02354
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                                                             7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LTDLKESHETITVWKAYDYTTENGIKYETQ-----GTRTQTFE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pamela Deneke
                                              16;
                                         Score 77.5; DE Pred. No. 4.1; 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTC-012
                                                                                   DB 4;
                                           50;
                                                                                 Length 468;
                                              Indels
                                           35;
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                                           Gaps
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12 NYPLTWRPDKQKLKRPYYRSLIQQ-----

-- LEQDILKNKLQKNTQLPSQRE. 56

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                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...823; SEQUENCE DESCRIPTION: SEQ ID NO: 5667: US-09-107-532A-5667
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                                                                                                                                                                                                           Query Match
                                                                                                                                                                         Matches
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Atent No. 6583275

GENERAL INFORMATION:

GENERAL LIFORMATION:

APPLICANT: Lynn A Dougette-Stamm and David Bush

APPLICANT: Lynn A Dougette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (781)893-82 INFORMATION FOR SEQ ID NO: 566 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR
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                                                                                                                                      14 QDAWKSLQQDQNKR-----YYLAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNATILYKN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSSFEECNKFVVP 128
                                ALLAGMPQAP-----SAYDPYV-----YPDQAKKRR---DTVLYTMLQNEKISQTEYD 309
                                                                  KHLTDLKESHETITVWKAYD-YTTENGIKYETQGTRTQTFEDVFVFSDYKNCDV-----
                                                                                                    QEAWMAVRLEQKKSKQEILTYYVNKVYMSNGLYGME----TASEMYFGKKLSELSLPQT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSDYKNCDVIFVP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LADYLDLNFT-TVGKAYKYGIEKGLLYTNIGSGTFISPNVFESITISTNEVTEHIIDFGL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- IFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: CD/ROM ISO9660
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                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 823 amino acids
                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                Enterococcus faecium
                                                                                                                                                                                       24.38;
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                                                                                                                                                                                       Score 77.5; DB 4; Pred. No. 9.1;
                                                                                                                                                                         Mismatches
                                                                                                                                                                         62;
                                                                                                                                                                                                         Length 823;
                                                                                                                                                                         Indels
                                                                                                                                                                         41;
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CURRENT FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2. Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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TYPE: PRT
ORGANISM: Bacillus thuringlensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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APPLICANT:
                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hass, G
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                APPLICATION NUMBER: FILING DATE: 08-APF
                                                                                                                                                                                                                         COUNTRY:
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 REGISTRATION NUMBER:
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5017703
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                                                                                                                                                                                                         98104
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                                                                                                                                                                                                                                                           Seattle
                                                                                                                                                                                                                                         Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09563269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DONOVAN, WILLIAM P.
                                                                                                                                                                                                                                                                            6300 Columbia Center,
                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                               Enfield,
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                                                                                                                                                                                                                                                                                              SEED and BERRY LLP
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                                                                                                                                                                       Floppy disk
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                                                                08-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                 Robert J.
David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.8%; Score 77;
24.3%; Pred. No.
                                                                                  US/08/824,692
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310 QAVNVP----VTDGLQELTQSDDN-TKIVD--NYVKEVINEVQEKTDKNVYTD
355
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268 TIHSDLIVNLKEDFAYEIIVKFENLSYSTLFNEDLFIYRFDKNHNLL-IEKTVGS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 QEKSQRNVLATIDYSKEGQAGKKYT-MMVTADQLATKIPG----YNPPPRVEQDRSHNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 QDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNATILYKNKHLTDLKESHETI 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 TVWK-----AYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNCDVIFVPKERGS 130
                                                                                                                                                                                                                                                                                                                                                           G. Michael
N: METHODS AND COMPOSITIONS FOR SCREENING
NO. FOR OR MODULATING A TUMOR ASSOCIATED ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLEOPTERAN-TOXIC POLYPEPTIDE COMPOSITIONS AND INSECT RESISTANT TRANSGENIC PLANTS
                                                                                                                                                                                                                                                          701 Fifth Avenue
Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 341;
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RESULT 8
US-09-071-035-396
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; TYPE: PRT
; ORGANIZM: Acinetobacter baumannii
US-09-328-352-6764
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US-09-328-352-6764
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TOPOLOGY:
US-08-824-692-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6754
                                                                                          Sequence 396, Application US/09071035 Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6764, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                       GENERAL INFORMATION:
APPLICANT: Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 19.5 ies 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          Match 7.6%;
Local Similarity 22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                              234 NMSHLTAHQEEWKKIIQVWDKTVKYINDPATHA------DAVKIMANRSGVDPKQYE 284
                                                                                                                                                                                                      285 LMVSGTHLLDINANKKVFTKSQGFDSIYGSSYHVNKFNVENGI-YKTE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 SPISQKIIYKEN------
                                                                                                                                                                                                                                           64 ILYKNKHLTDLKESHETITVWKAYD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 SLQQDQNKRYYLAQATQ------TTDGVWGEEF-TCVSVTAEK---IGK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 SSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWGKEKPKCVEISCKSPDVING
                                                                                                                                                                                                                                                                                                                    6 NEAKLGSYQDAWKSLQQ--DQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNAT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WIPAP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKSCDNPYIP-----NGDYSPLRIKHRTGDEITYQCR--NGFYPATRGNTAK--CTSTG 201
                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                    Enterococcus faecalis Polynucleotides and Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                        Score 75.5; Di
Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130001.404
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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                                                                                                                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                           -YTTENGIKYETQ 100
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                                                                                                                                                                                                                                                                                                                                                         Indels
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; TOPOLOGY: lir
; MOLECULE TYPE:
US-09-071-035-396
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                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-071-035-358
                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                               Sequence 358,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Gil H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                        OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                             CLASSIFICATION:
                                                                                                                                                                                                    STREET: 9410 Key
CITY: Rockville
STATE: Maryland
                                                                                                                           COMPUTER:
                                               FILING DATE:
                                                             APPLICATION NUMBER:
                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 LYKNKHLTDLKESHETIT 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                               -VNGKHNEDLKEKSQTLT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maryland
                                                                                                                                                                                                                                     E: Human Genome Sciences,
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                   Application US/09071035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 amino acids
                                                                                                                                                                                                                                                                                                                    Gil H. Choi
                                                                                                                                                                                         USA
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                                                                                                                        HP Vectra 486/33
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28.2%;
                                                                                                           MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                    Enterococcus faecalis Polynucleotides and Polypeptides
                                                             us/09/071,035
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                                                                                                                                         3.50 inch, 1.4Mb storage
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Pred. No. 8.
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8.5;
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; MOLECULE TYPE: US-09-071-035-394
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US-09-071-035-394
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; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301)
INFORMATION FOR SEQ ID NO: 351
SEQUENCE CHARACTERISTICS:
SEQUENCE TRACTH: 1074 amino acids
                                                                                                                 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ent No. 644804
                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                               REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PREFERENCE/DOCKET NUMBER: PREFERENCE/DOCKET NUMBER: 0.001
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS ve.
SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Rockville
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                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 LYKNKHLTDLKESHETIT 82
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                                                                                                                                                                                                               A. Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EE: Human Genome Sciences, Inc
9410 Key West Avenue
                                                                              1074 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. Cho1
                                            single
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                                                                                                                                                                                                                                                                                                                                                                                          MSDOS version 6.2
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                                                                                                                 394:
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Pred. No. 25;
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US-09-198-452A-1120
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US-09-634-238-229
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                             ; NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ FOR
SEQ ID NO 229
LENGTH: 771
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
JS-09-634-238-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1120
LENGTH: 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr TITLE OF INVENTION: and treatment of infection
                                                                                                                    CURRENT APPLICATION NUMBER: US/09/634,238 CURRENT FILING DATE: 2000-08-08
                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                    TITLE OF INVENTION: Polynucleotides,
                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                         tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 28.4%;
                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          993 -VNGKHNEDLKEKSQTLT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                940 GTNKEIWKSGKIEHEVNDKEFTKTVLAEKVDTGKYPEGTKFTFTEINYEKDGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 DAGLYAYNHNLDSSPEFYETIITTRSYEDRLNTLDVVNKSGI 190
                                                                                                                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 LYKNKHLTDLKESHETIT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 GSYQDAWKS--LQQDQNKRYY----LAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNATI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NATILYKNKHLTDLKESHETITVWKAY------DYTTENGI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 ANEAKLGSYQDAWKSLQQDQNKRYY---LAQATQTTDGVWGEEFTC-VSVTAEKIGKKKL 60
                                                                                                                                                                                                                                                                                                                                                                                                         '9, Application US/09634238
6544772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATRVCLGA---AWRNAKDD---RYFDRVLAMVKSITD--LGAEVCCALGMLSEEQAKKLY 148
                                                                                   FastSEQ for Windows Version 4.0
                                                                                                                                                                                                       Coolbear, Timothy
                                                                                                                                                                                                                                            Holland, Ross
O'Toole, Paul W.
                                                                                                                                                                                                                        Reid, Julian R.
                                                                                                                                                                                                                                                                               Christensson, Anna C.
                                                                                                                                                                                                                                                                                              Lubbers, Mark W.
Dekker, James
                                                                                                                                                                                                                                                                                                                                 Havukkala, Ilkka J.
Bloksberg, Leonard, N.
                                                                                                                                                                                                                                                                                                                                                                      Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                       11000.1043U1
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Pred. No. 5.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                      materials incorporating for using them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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US-09-634-238-262
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                  SEQ ID NO 23258
LENGTH: 144
                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                             Sequence 23258, Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 262
LENGTH: 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Best Local
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                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                          APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS #
                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/634,238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION: Polynucleotides, materials inco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                               620 KPTSHGISYAEQTISQKIYKALMSYT---
                                                                                                                                                                                                                                                                                                                                                                                                            571 YQAGKTGTTD--YSDE-----ELKQNPALNATGIAKDAWFTGYTR-NRVISVWTGYD 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262, Application US/09634238
). 6544772
                                                                                                                                                                                                                                                                                                                                                                                                                                          29 YLAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNATILYKNKHLTDLKESHETITVWKAYD 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 YLAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNATILYKNKHLTDLKESHETITVWKAYD 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                            YTTENGIKYETQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSDEGDYELWVSEDKID 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTTENGIKYETQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSDEGDYELWVSEDKID 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holland, Ross
O'Toole, Paul W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dekker, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mark W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Timothy
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74; DB Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
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                                                                                                                                                                                 AND
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                                                                                                                                                                                                RELATING TO PSEUDOMONAS
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                                                                                                                                                                                                                                               US-08-961-083-80
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US-08-961-083-80
                                                                                                                                                                                 Matches
                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 9410 Ke
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                156 FDYKWNMGWMNDILRFYEEDPIYRKYDFNLVTFSFMYVXKENYLLPFSHDEVVHGKKSMM
                  97
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5. 6159469
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27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20850
                                                                                                                                                                                                                                                                                                              amino acid
                YETQGTRTQTFEDVFVFSDYKNC----DVIFVPKERGSDEGDYELWVSEDKID--KIPDC 150
                                                                               ATILYKNKHLTDLKESHETITVWKAYDYTT---
                                                                                                                                             YQDA-WKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEK-----IGKKK---LN 61
                                                                                                               YDDAPWTPNKDGGNLNYEGYYFLQRLNEVIKLEYPDVMMIAEESSSAIKITGMKEIGGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTAKAPAGKRARKVKQYKNPHTGEVIETKGGNHKTLKEWKA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maryland
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26.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          version 6.2
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                                                                                                                                                                                                                                                                                              Description
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Use of histacalin proteins for treating or preventing non-infective conjunctivitis, or for manufacturing a medicament for treating or preventing conjunctivitis, e.g. seasonal or perennial allergic conjunctivitis
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Listeria monocytog
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Listeria monocytog
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Listeria monocytog Bacillus thuringie Candida albicans Listeria monocytog Ragweed allergen 1 Human secreted pro

ALIGNMENTS

01-SEP-1999; 08-MAR-2001. WO200115719-A2 Unidentified. Histacalin; MS-HBP1; conjunctivitis. AAB74290; Nuttall PA, Paesen GC; 24-AUG-2000; 2000WO-GB03282. Histacalin protein MS-HBP1 20-JUN-2001 AAB74290 standard; (EVOL-) EVOLUTEC LTD. 2001-257675/26. (first entry) 99GB-0020674. protein; 182 ξ

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RESULT 2
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                     The present invention relates to a method for treating or preventing allergic rhinitis. The method involves employing a blood-feeding ectoparasite-derived (e.g. tick-derived) histacalin protein. The presequence is one such histacalin protein. The histacalin protein, is useful for treating or preventing allergic rhinitis, both seasonal apperennial allergic conjunctivitis.
                                                                                                                                                                                                                            Use of histacalin proteins for treating or preventing allergic rhinitis, or for manufacturing a medicament for treating or preventing allergic rhinitis, e.g. seasonal or perennial allergic rhinitis
                                                                                                                                                                                        Disclosure;
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                                                                                                                                                                                      Pages 4-6;
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allergic rh
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                                                                                                                                                                                    19pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in; antiinflammatory;
rhinitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 989;
Pred. No. 3
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3.1e-94;
es 0;
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                                               seasonal and
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                             New vasoactive amine binding proteins and related nucleic vectors - transformed cells and transgenic animals, used f assaying or removing histamine and as antihistamine or anti-inflammatory agents
                                                                                                             WPI; 1998-018506/02.
N-PSDB; AAV00229.
                                                                                                                                         Nuttall PA,
                                                                                                                                                                                                                                                                                                                                    histamine; serotonin; assay; antil insect bite; snake bite; scorpion transgenic animal; tick.
                                                                                                                                                                                                                                                                                                                                             Male-specific vasoactive amine binding proto
histamine; serotonin; assay; antihistamine;
insect bite; snake bite; scorpion bite; derr
                                                                                                                                                                                                                                                                                                                                                                                   Tick
                                                                                                                                                                             18-APR-1997;
18-MAY-1996;
                                                                                                                                                                                                                                            WO9744451-A2
                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                        19-MAY-1997;
                                                                                                                                                                                                                          27-NOV-1997.
                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                    Rhipicephalus
                                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                       AAW37448;
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                                                                                                                                                         (OXFO-)
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Similarity . 100.0%;
82; Conservative
                                                                                                                                                          OXFORD
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                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                          VACS LTD.
                                                                                                                                                                             97GB-0007844.
96GB-0010484.
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                                                                                                                                                                                                                                                                     /label= Sig_peptide 79..81
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                         GC;
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                                                                                                                                                                                                                                                                                                                                                                                  protein 1 MS-HBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 989; DB 22;
Pred. No. 3.1e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                       protein 1; MS-HCP1;
mine; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                               dermatitis;
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This protein comprises tick Rhipicephalus appendiculatus (Ra) no male-specific histamine binding protein 1 (MS-HBP1). Its amino acid sequence was deduced from a cDNA clone (see AAV00227) obtain from a salivary gland cDNA library. Female-specific HSP1 and

) obtained and

novel

Example

2;

Fig

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AAY1800 AAY180
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CC from Dermacenter reticularis, were also identified. These novel
CC vasoactive amine binding proteins (VABPs) can be expressed in
CC bost cells using e.g. a baculovirus expression system. They can
CC be used: (i) to assay histamine (or other VA such as serotonin) in
CC body fluids or cell culture supernatants, e.g. to monitor the
CC effect of allergens; (ii) for binding VA, e.g. to remove histamine or
CC from blood, food, cell cultures etc.; (iii) as an antihistamine or
CC anti-inflammatory agents, e.g. for treating insect, snake or
CC corpion bites or dermatitis, or as a carrier for slow release of
CC statamine-related compounds; (iv) in vaccines to protect against
CC metazoan parasites, especially in animals; (v) as reagents for
CC studying inflammation, involvement of VA in ulcer formation or the
CC immune response etc. VABPs provide a more sensitive assay for
CC histamine than low-affinity antibodies currently used. They may
CC also be more effective and safer than conventional antihistamines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergtc rhinitis; atopic dermatitis; food allergy; doubting allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator;
                                                         Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Histamine binding protein MS-HBP1.
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                                                                                                                                                                          26-JUN-1998;
26-NOV-1997;
                                                                                                                                                                                                                                                               26-NOV-1998;
                                                                                                                (OXFO-) OXFORD
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182; Conserv
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ilarity 100.0%;
Conservative (
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                                                                                                                VACS LTD
                                                                                                                                                                          98GB-0013917
97GB-0025046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             blood-sucking ectoparasite;
                                                                                                                                                                                                                                                               98WO-GB03530
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Pred. No. 3.5e-94;
; Mismatches 0;
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Matches 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used as components of vaccines directed against blood-sucking also be used as components of vaccines directed against blood-sucking
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                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Histacalin; FS-HBP1; conjunctivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Histacalin
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                                                                                                          Nuttall PA,
                                                                                                                                                                                                                                                                   24-AUG-2000; 2000WO-GB03282
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Pred. No. 3.5e-94;
; Mismatches 0;
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Use of histacalin proteins for treating or preventing non-infective

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Best Local S
Matches 74
                                   The present invention relates to a method for treating or preventing allergic rhinitis. The method involves employing a blood-feeding ectoparasite-derived (e.g. tick-derived) histocalin protein. The presequence is one such histocalin protein. The histocalin protein, is useful for treating or preventing allergic rhinitis, both seasonal are
                                                                                                            Disclosure;
                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                              rhinitis,
                                                                                                                                                                                                                                                                              24-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                         FS-HBP2; histacalin protein; antiinflammatory; antiallergic; opthalmological; allergic rhinitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conjunctivitis, or for manufacturing a medicament for treating preventing conjunctivitis, e.g. seasonal or perennial allergic conjunctivitis
                                                                                                                                                                                                          Nuttall
                                                                                                                                                                                                                                 (EVOL-)
                                                                                                                                                                                                                                                        01-SEP-1999;
                                                                                                                                                                                                                                                                                                       08-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                               Histacalin protein FS-HBP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e present invention relates to the use of a histacalin protein r treating or preventing conjunctivitis. The present sequence the histacalin protein FS-HBP1. The invention is particularly the treatment of allergic or seasonal conjunctivitis.
                                                                                                                              of histacalin proteins for treating or preventing allergic nitis, or for manufacturing a medicament for treating or preventing ergic rhinitis, e.g. seasonal or perennial allergic rhinitis
                                                                                                                                                                                  2001-218521/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQAEFLEMNNADTNMQFATEKVTAVKMYGYNRENAFRYETED---GQVFTDVIAYSD-DNC
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                          allergic
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                          conjunctivitis
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Pred. No. 3.6e
29; Mismatches
                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                           allergic rhinitis, both season
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No. 3.
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tes 62;
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Best Local S
Matches 74
This protein comprises tick Rhipicephalus appendiculatus (Ra) novel female-specific histamine binding protein 2 (FS-HBP2). Its amino acid sequence was deduced from a cDNA clone (see AAV0022B) obtained from a salivary gland cDNA library. FS-HSP1 (see AAW37446) and male-specific HSP1 (see AAW37448) and a related protein, D.RET6 (see AAW37449) from Dermacenter reticularis, were also identified. These novel vasoactive amine binding proteins (VABPs) can be expressed in host cells using e.g. a baculovirus expression system. They can be used: (i) to assay histamine (or other VA such as serotonin) in body fluids or cell culture supernatants, e.g. to monitor the effect of allergens; (ii) for binding VA, e.g. to remove histamine
                                                                                                                                                                                           New vasoactive amine binding proteins and related nucleic acid, vectors - transformed cells and transgenic animals, used for assaying or removing histamine and as antihistamine or anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          histamine; serotonin; assay; insect bite; snake bite; scor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tick vasoactive
                                                                                                                                                                  Example
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18-MAY-1996;
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                                                                                                                                                                  Fig 2; 44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               animal; tick.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.5%;
                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scorpion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
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Pred. No. 3.6e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mine binding protein 1; FS-HCP1;
antihistamine; anti-inflammatory;
rpion bite; dermatitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
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les 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                          Histamine binding protein; serotonin binding compound; inflammation; Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; gasthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; asthma; urticaria; allergic rhinitis; psychological disorder; vaccine; psychological disorder; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-inflammatory agents, e.g. for treating insect, snake or scorpion bites or dermatitis, or as a carrier for slow release of histamine-related compounds; (iv) in vaccines to protect against metazoan parasites, especially in animals; (v) as reagents for studying inflammation, involvement of VA in ulcer formation or the immune response etc. VABPs provide a more sensitive assay for histamine than low-affinity antibodies currently used. They may also be more effective and safer than conventional antihistamines
This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine
                                                            Claim
                                                                                  of allerg
                                                                                               Histamine
                                                                                                                                    HPI;
                                                                                                                                                         Nuttall PA,
                                                                                                                                                                                                       26-JUN-1998;
26-NOV-1997;
                                                                                                                                                                                                                                                                  03-JUN-1999
                                                                                                                                                                                                                                                                                         W09927104-A1
                                                                                                                                                                                                                                                                                                               Rhipicephalus
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                                                                                                                                 1999-357841/30.
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                                                                                                                                                                                                                                                                                                                                       repair;
                                                                                                                                                                                OXFORD
                                                                                                                       AAX76965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                           F1g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | IQAEELEMNNADTNMQFATEKYTAVKMYGYNRENAERYETED--GQVFTDVIAYSD-DNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVIYVPGTDGNEEG-YELWTTD--YDNIPANCLNKFNEYAVGRE--TRDVFT-SAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSC
                                                                                     1es
                                                                                               and serotonin
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                                                                                                                                                         Paesen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą,
                                                                                                                                                                                                                                                                                                                                     blood-sucking
                                                                                                                                                                                VACS
                                                                                                                                                                                                      98GB-0013917.
97GB-0025046.
                                                                                                                                                                                                                                          98WO-GB03530
                                                          84pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell cultures etc.; (iii) as an antihistamine or agents, e.g. for treating insect, snake or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                         ဂ္ဂ
                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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                                                           English.
                                                                                            binding
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Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                     ectoparasite;
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                                                                                             compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2e-26;
nes 62;
                                                                                                useful
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                                                                                               the
                                                                                             treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190;
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RESULT 9
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking
                                                                               Claim 4;
                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB74288 standard;
                                                                                                     preventing conjunctivitis, e.g. seasonal or conjunctivitis -
                                                                                                                          Use of histacalin proteins for treating or preventing conjunctivitis, or for manufacturing a medicament for
                                                                                                                                                                                                                                  01-SEP-1999;
                                                                                                                                                                                                                                                        24-AUG-2000;
                                                                                                                                                                                                                                                                              08-MAR-2001
                                                                                                                                                                                                                                                                                                     WO200115719-A2.
                                                                                                                                                                                                                                                                                                                                                 Histacalin;
                                                                                                                                                                                                                                                                                                                                                                       Histacalin
                                                                                                                                                                                                                                                                                                                                                                                                                      AAB74288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                           (EVOL-) EVOLUTEC LTD
                                                                                                                                                              2001-257675/26
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                                                                                                                                                                                     PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVIXVPGTDGNEEG-YELWTTD--YDNIPANCLNKFNEYAVGRE--TRDVFT-SAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK 59
                                                                               Page 5-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQAEFLEMNNADINMQFATEKVTAVKMYGYNRENAFRYETED--GQVFTDVIAYSD-DNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDEKS
                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 AA;
                                                                                                                                                                                                                                                                                                                                                 FS-HBP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                     Paesen
                                                                                                                                                                                                                                                        2000WO-GB03282.
                                                                                                                                                                                                                                  99GB-0020674
                                                                            19pp;
                                                                                                                                                                                                                                                                                                                                                                        FS-HBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.5%;
                                                                                                                                                                                                                                                                                                                                                 conjunctivitis
                                                                               English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                             172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 331.5; DB 2
.pred. No. 4.2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                               perennial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                                               y non-infective
r treating or
l allergic
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Query Match Best Local Similarity

39 39

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Score Pred.

267.5; No. 1.0

.6e-19;

22;

Length

Sequence

172

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The present invention relates to the use of a histacalin protein for treating or preventing conjunctivitis. The present sequence is the histacalin protein FS-HBPI. The invention is particularly in the treatment of allergic or seasonal conjunctivitis.

useful

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120 YVIYALGPDGSGAG-YELWAT-DYTDVPASCLEKFNEYAA---GLPVRDVYT-SDCLP 171

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AAB73260
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                                                                                                                                                  Matches
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                         allergic rhinitis. The method involves employing a blood-feeding ectoparasite-derived (e.g. tick-derived) histacalin protein. The sequence is one such histacalin protein. The histacalin protein, useful for treating or preventing allergic rhinitis, both season perennial allergic conjunctivitis.
                                                                                                                                                                                                                                                                                                                                        Use of histacalin proteins for treating or preventing allergic rhinitis, or for manufacturing a medicament for treating or preventing rhinitis, e.g. seasonal or perennial allergic rhinitis
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                         The present invention relates to a method for treating
                                                                                                                                                                                                                                                                                                                                                                                                                          Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FS-HBP1; histacalin protein; antiinflammatory; antiallergic; opthalmological; allergic rhinitis.
                                                                                                                                                                                                                                                                                                                  Disclosure; Pages 4-6; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200116164-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histacalin protein FS-HBP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 - AUG - 2000;
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                                                                                                                                                             Local
120 DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSCKP 177
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                                                                                                                                                             Similarity
                                                          LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNC
                                      VEAWFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTED--GQVLTDVLAFSD-DNC
                                                                                        PVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKN 62
                                                                                                       PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVIYALGPDGSGAG-YELWAT-DYTDVPASCLEKFNEYAA---GLPVRDVYT-SDCLP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSCKP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEAWFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTED--GQVLTDVLAFSD-DNC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVWADZAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDEKN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK 59
                                                                                                                                                                                                   172
                                                                                                                                               Conservative
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                                                                                                                                                           27.0%;
                                                                                                                                               20;
                                                                                                                                            Score 267.5;
Pred. No. 1.6e
20; Mismatches
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                                                                                                                                           ..6e-19;
nes 77;
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                                                                                                                                                                      22;
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                                                                                                                                                                        172;
                                                                                                                                                                                                                                       seasonal
                                                                                                                                                                                                                                                                                        preventing
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                                                                                                                                                                                                                                                                                                                                                       preventing
                                                                                                                                            Gaps
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RESULT 11
AAW37446
                                from a salivary gland cDNA library. FS-HSP2 and male-specific
HSP1 (see AAW37447-48) and a related protein, D.RET6 (see AAW37449)
Cfrom Dermacenter reticularis, were also identified. These novel
crown because the binding proteins (VABPs) can be expressed in
thost cells using e.g. a baculovirus expression system. They can
be used: (1) to assay histamine (or other VA such as serotonin) in
the body fluids or cell culture supernatants, e.g. to monitor the
ceffect of allergens; (ii) for binding VA, e.g. to remove histamine
ceffect of allergens; (ii) for binding VA, e.g. to remove histamine
ceffect of allergens; (ii) for binding VA, e.g. to remove histamine
ceffect of allergens; (ii) for binding VA, e.g. to remove histamine
ceffect of allergens; (ii) for treating insect, snake or
anti-inflammatory agents, e.g. for treating insect, snake or
scorpion bites or dermatitis, or as a carrier for slow release of
histamine-related compounds; (iv) in vaccines to protect against
metazoan parasites, especially in animals; (v) as reagents for
studying inflammation, involvement of VA in ulcer formation or the
immune response etc. VABPs provide a more sensitive assay for
histamine than low-affinity antibodies currently used. They may
also be more effective and safer than conventional antihistamines.
                                                                                                                                                                                                                                                                                                                                                                     This protein comprises tick Rhipicephalus appendiculatus (Ra) novel female-specific histamine binding protein 1 (FS-HBP1). Its amino acid sequence was deduced from a cDNA clone (see AAV00227) obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vasoactive amine binding proteins and related nucleic vectors - transformed cells and transgenic animals, used fassaying or removing histamine and as antihistamine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-018506/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Female-specific vasoactive amine binding protein 1; FS-HCP1; histamine; serotonin; assay; antihistamine; anti-inflammatory; insect bite; snake bite; scorpion bite; dermatitis; vaccine; transgenic animal; tick.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 1; 44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuttall PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-1997;
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96GB-0010484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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Query Match Matches

Local

Similarity 70; Conserv

Conservative

20;

27.0%;

Score 267.5; Pred. No. 1. Mismatches

1.8e-19; hes 77; DB 19;

Indels Length

Gaps

7;

190; 11;

Sequence

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    Query Match
Best Local Similarity
Matches 70; Conserv
                                                                                               This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.
                                                           Sequence
                                                                                         ectoparasites.
                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 84pp; English.
                                                                                                                                                                                                                                                                                                                         Histamine and serotonin binding compounds useful for the treatment of allergies
                                                                                                                                                                                                                                                                                                                                                                                                             Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                           (OXFO-)
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26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEAWFMFMNNADTVYQHTFEKATPDKMYGYNKENAITYQTED--GQVLTDVLAFSD-DNC
                                                             190
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97GB-0025046.
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                27.0%;
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    Score 267.5;
Pred. No. 1.8e
20; Mismatches
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.8e-19;
77;
                                DB
                               20;
                             Length
                                190;
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Conservative

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                                          library. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergie rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.
                                                                                                                                                                                                                                   This sequence
                                                                                                                                                                                                                                                                                                 of allergies
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N-PSDB; AAX76971.
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                                vaccines
                                                                                                                                                                                                 This sequence is an example of a histamine or serotonin binding compound (A), of the invention. cDNA encoding this sequence was i from a mixed Bophilus microplus/Ixodes hexagonus cDNA expression
                                                                                                                                                                                                                                                                                                                                                                                             Nuttall
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26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVIYALGPDGSGAG-YELWAT-DYTDVPASCLEKFNEYAA---GLPVRDVYT-SDCLP
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97GB-0025046.
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                                                                                                                                                                                                                                                                                                               binding
                              The molecules may blood-sucking ecto
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                                                                                                                                                                                                                                                                                                                 compounds useful for the treatment
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Best Local
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           This sequence is an example of a histamine or serotonin binding compound (A), of the invention. cDNA encoding this sequence was isolated from a mixed Boophilus microplus/Ixodes hexagonus cDNA expression library. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of
                                                                                                                                                                                                                                                                             Histamine and serotonin binding compounds useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator;
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26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Histamine binding protein; serotonin binding compound; inflammation;
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                                                                                                                                                                                                                                                                  allergies
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DB; AAX76970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTA----EKIGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDVLYIPYKEDG-----YELWVRSEYLQNTPTCCQFIFDLVA--LGRTTYNIST 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDVIFVP-KERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKN 118
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                                                                                                                                                                                                                                   7;
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97GB-0025046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     blood-sucking ectoparasite; therapy.
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                                                                                                                                                                                                                                84pp;
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Pred. No. 2.2e-19;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                  New vasoactive amine binding proteins and related nucleic vectors - transformed cells and transgenic animals, used assaying or removing histamine and as antihistamine or
                                                                                         anti-inflammatory agents
                                                                                                                                                                      Nuttall PA, Paesen
                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                     Example
                                                                                                                                                                                                                                                                                                                                                                             Vasoactive amine binding protein; D.RET6; histamine; serotonin; assay; antihistamine; anti-inflammatory; insect-bite; snake bite;
                                                                                                                                                                                                                                                                                                                                                                                                           Tick vasoactive amine binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW37449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW37449 standard; Protein; 209
                                                                                                                                                                                            (OXFO-) OXFORD VACS LTD
                                                                                                                                                                                                                18-APR-1997;
18-MAY-1996;
                                                                                                                                                                                                                                              19-MAY-1997;
                                                                                                                                                                                                                                                                  27-NOV-1997.
                                                                                                                                                                                                                                                                                     WO9744451-A2
                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                     scorpion
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                                                                                                                                                     1998-018506/02.
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                                                                                                                                                                                                                                                                                                                                                                     bite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNIST 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKKLNATILYKN------KHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNVYT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVEYNTT - - YKNQSQQWVSMTENVTAVQE - - EGYDVKNIIQWTTENNTK - - - - - - - F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTA----EKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDTVVFTDGQTCDLLYIPYKENG----YELWVRSDYLQNTPTCCQFIFDLVA--LGRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDVFVFSDYKNCDVIFVP-KERGSDEGDYELWYSEDKIDKIPDCCKFTMAYFAQQQEKTV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTTW-HSKELKNYQDAWKSINQNVSTTYYFLRSTYNNDSYWGKNFTCLSVTVTSKHESTF
                                                                   Fig 4; 44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 AA;
                                                                                                                                                                                                                                                                                                                                                 reticularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                               97GB-0007844.
96GB-0010484.
                                                                                                                                                                                                                                                                                                                                                                     dermatitis;
                                                                                                                                                                                                                                              97WO-GB01372
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.6%;
                                                                                                                                                                                                                                                                                                       Sig_peptide
                                                                    English
                                                                                                                                                                                                                                                                                                                                                                    vaccine; transgenic animal; tick.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                           protein D.RET6
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.8e-19;
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This protein comprises tick Dermacenter reticularis (Dr) novel vasoactive amine binding protein (VABP) D.RET6. Its amino acid sequence was deduced from a CDNA Clone (see AAV00230) obtained from a Dr salivary gland cDNA library. 3 Novel VASPs, designate of the control of the c

sequence was deduced and cDNA library. 3 Nover from a Dr salivary gland cDNA library. 3 Nover FS-HBP1, FS-HBP2 and MS-HBP1 (see AAW37446-48),

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Search completed: August 1, 2003, 12:22:49 Job time: 57.5067 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VABPs can be expressed in host cells using e.g. a baculovirus cexpression system. They can be used: (i) to assay histamine (or other VA such as serotonin) in body fluids or cell culture supernatants, e.g. to monitor the effect of allergens; (ii) for binding VA, e.g. to remove histamine from blood, food, cell cultures etc.; (iii) as an antihistamine or anti-inflammatory agents, e.g. for treating insect, snake or scorpion bites or dermatitis, or as a carrier for slow release of histamine-related compounds; (iv) in vaccines to protect against metazoan parasites, especially in animals; (v) as reagents for studying inflammation, involvement of VA in ulcer formation or the immune response etc. VABPs provide a more sensitive assay for histamine than low-affinity antibodies currently used. They may also be more effective and safer than conventional antihistamines.
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.4%; Score 251.5; DB 19; Length 209; Best Local Similarity 35.3%; Pred. No. 9.3e-18; Matches 61; Conservative 29; Mismatches 66; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                            113 FSDYKNCDVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTWAYFAQQQEKT 165 |:| :|| :|| :|| :|| :|| 145 FTDGELCDVFYVP---NADQG-CELWVKKSHYKHVPDYCTFVFNVFCAKDRKT 193
                                                                                                                                                                                                                        88 EDYTVTSVFTFRNAS-SPIKYYNVTETVKAVFQYGYKNIRNAIEYQVGGGLNIT--DTLI 144
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Minimum DB :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Best Local S
Matches 66
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Sangamnadech S., Paesen G.C., Nuttall P.A.;
Sangamnadech S., Paesen G.C., Nuttall P.A.;
Sangamnadech S., Paesen G.C., Nuttall P.A.;
A high affinity serotonin- and histamine-binding lipocalin secreted by blood-feeding ticks.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

"EMBL; AF217101; AAL56644.1; -.

"EMBL; AF217101; AAL56644.1; -.

"InterPro: IPR002970; His_binding.1

Pfam; PF02098; His_binding; 1.

"FF01859591 CRC64;

"FF01864; 23889 MW; E5EBBBE710859591 CRC64;
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|--|---|--|--|
| 81.5<br>81.5<br>81.5   | 82.5<br>82.5<br>81.5<br>81.5  | 83 85.55<br>83.55<br>83.55<br>83.55<br>83.55   | 86.5<br>86.5<br>86.5<br>86.5<br>86.5   |
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| 1129<br>1956<br>3597<br>1263   | 220<br>496<br>419<br>374<br>897   | 573<br>617<br>686<br>1237<br>1612<br>2488<br>4494<br>601   | 606<br>377<br>3381<br>193<br>254<br>723<br>723<br>736<br>736<br>6077   |
| 11 5 5   |   | 22556865   | 16<br>16<br>16<br>16   |
| Q9VPP3<br>Q8IIE1<br>Q8ILR5<br>Q9QYZ2   | Q8MVB8<br>Q9GSW0<br>Q9FJH4<br>Q8CX67<br>Q8ID14<br>Q8L2H9  | Q8IDM2<br>Q8XII6<br>Q8MGG0<br>Q92CG8<br>Q8Y591<br>Q8I3R5<br>Q8I3R5<br>Q8I3R5<br>Q8I3R5<br>Q8I3R5<br>Q8I3R5 | Q977Y3<br>Q9QB34<br>Q8IDK4<br>Q9IBS3<br>Q23871<br>Q8P1H6<br>Q9A0E7<br>Q8K7Z8<br>Q8ICS6<br>Q8ICS6   |
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## ALIGNMENTS

O8WSK7 PRELIMINARY; PRT; 209 AA.

O8WSK7;
O1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Serotonin and histamine binding protein.

update)

Dermacentor reticulatus.

Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;

Parasitiformes; Ixodida; Ixodidae; Dermacentor.

NCBI\_TaxID-57047;

Acari;

| 7; Length 209; 7; Length 209; 7; Todels 12; Gaps 69; Indels 12; Gaps DP-VWGNDFTCVGVMANDVNEDEK | A QY 118 NCDVIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEY-AVGRETRDVFTSACL 170 | Qy 62 SIQAEFLEMNNADTNMQFATEKVTAVKMYGY-NRENAFRYETEDGQVFTDVIAYSD-D 117 um :::    :::           | Oy 3 PDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDP-VWGNDFTCVGVMANDVNEDEK 61 | Utery Match 30.1%; Score 282; DB 5; Length 209; Best Local Similarity 37.5%; Pred. No. 5.2e-17; Matches 66; Conservative 29; Mismatches 69; Indels 12; Gaps |
|---|---|--|--|---|
|   | NIPANCLNKENBY-AVGRETRDVFTSACL 170 ::       :   :   :   :            | \VKMYGY-NRENAFRYETEDGQVFTDVIAYSD-D    .           : ::  :  VFQYGYKNIRNAIEYQVGGGLNITDTLIFTDGE | YMVKATYKNDP-VWGNDFTCVGVMANDVNEDEK                                    | 882; DB 5; Length 209;<br>Vo. 5.2e-17;<br>matches 69; Indels 12; Gaps   |

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RESULT COMMVC2
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                                                                MEDIINE-22255705; PubMed-12368864; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdya A.B., Martin D.M.A., Frairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O8IL35; PRELIMINARY;

O8IL35; O1-MAR-2003 (TrEMBLrel. 23,

O1-MAR-2003 (TrEMBLrel. 23,

O1-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBMVC2;
O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative secreted histamine binding protein.
Ixodes scapularis (Black legged tick) (Deer tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein, PF14_0414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Rhode Island; TISSUE-Salivary Valenzuela J.G., Francischetti I.M., Mather T.N., Ribeiro J.M.C.; "Exploring the Sialome of the Tick Ve scapularis.";
                       "Genome sequence falciparum.";
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6945;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
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419:498-511(2002)
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Pham V.M.,
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                                                 Plasmodium
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Best Local
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Pfam; PF02324; Glyco_hydro_70;
Glycosyltransferase; Signal; T1
SIGNAL 1 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato S., Inoue M., Handa N., Aizawa Y., I

"DNA sequence of the glucosyltransferase

Streptococcus sobrinus.";

DNA Seq. 4.19-27(1993).

EMBL; D13858; BAA02976.1; -

InterPro; IPR002479; CW_binding.

InterPro; IPR003318; GN_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 21, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Glucosyltransferase-I precursor (EC 2.4.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE014823; AAN37027.1;
Hypothetical protein.
SEQUENCE 1898 AA; 223829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-OMZ176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
NCBI_TaxID=1310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bactería; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus sobrinus
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                                              139
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490
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                                                                                                                                                                                                                                                                                335 QPQWNGESEKPYDDHLQNGALLFDNQTDLTPDTQSNYKLLNRTPTNQTGSLDSRFTYNPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        571 AWKNSSYLVEE---YCKSKYENKKDKLIIDNYDNSLFT--HIYSN--NHDSKEEQSNFFF
                                                                                                                                         87
                                                                                                                                                                                                                39 DPVWGNDFTCVGVMANDVNEDEKSIQAEFL-----
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                                                                                                                                                                                                                                                                                                                                                                           l Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
                                                                                                                                                                                                                                                                                                                            2 QPDW-----ADEAANGAHQ-DAWKSLKADVENVYYMV------KATYK-N 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 27.9
44; Conservative
                                                                                                                                                                                     DPLGGYDF----LLANDVDNSNPVVQAEQLNWLHYLLNFGSIYANDADAN--FDSIRVDA
                                                                                                                                       VKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCDVIYVPGTDGNEEG-----YELWT- 138
NDTPYLHDDGDNL-MNMDNKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYDN-KIVLNDFYKGIQTLFKKKYYDYDNIFSVCINNYRQ
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                                            -----TDYDNIPANCINKF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1590 AA;
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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38 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                               11.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DTNMQFATEKVTAVKMYGYNR--ENAFRYETEDGQVFTDVI----AY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactobacillales; Streptococcaceae;
                                                                                          -DNVDADLLQISSDYLKAAY--GIDKNNKNANNHVSIVEAWSD 489
                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
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                                                                                                                                                                                                                                                                                                                                                                         Score 103; DB Pred. No. 3.2; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 104.5;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLUCOSYLTRANSFERASE-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C3C83A57CF3C2B0E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --ISKYFYPRISYKKFSYDTFEGEKFDNLILGGMCY
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e gene of serotype o
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                                                                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                    ----FMNNADTNMQFATEKVTA 86
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1590;
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Best Local
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Q55263;
Q1-NOV-1996 (Tremblre
01-JAN-1998 (Tremblre
01-CCT-2002 (Tremblre
GTF-I,
                                                                                              STRAIN-RIJ3;
STRAIN-RIJ3;
Katrib M.T., Davies N.P., Stewart T.S.;
**Unique Insert Sequences Within Carbamoyl Phosphate Synthetase From Plasmodium berghei and Plasmodium chabaudi.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) - RCHO + NH(2)O + O(2) - RCHO + NH(2)O + O(2) - RCHO + NH(2)O + O(3)O + O(4)O + O(5)O + O(5)O + O(6)O + O(6)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "DNA and amino-acid sequences of water-insoluble-glucan synthetase produced from Streptococcus sobrinus ATCC 33478.";
Ann. Kagoshima Univ. Dental School 16:23-29(1996).
EMBL; D63570; BAA09792.1; -.
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 15.
Pfam; PF012324; Glyco_hydro_70; 1.
SEQUENCE 1590 AA; 176058 MW; 9DF7A3F2C6E4FD43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus sobrinus. Bacteria; Firmicutes; L
                                                                                                                                                                                                                                                                                                               Plasmodium berghei.
Eukaryota; Alveolata;
NCBI_TaxID=5821;
     EMBL;
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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SIMILARITY).
SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE
L; AF286897; AAG10785.1; -.
                                                                  H(2)O(2).
COFACTOR: BINDS 1 COPPER ION
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8 (TrEMBLrel.
2 (TrEMBLrel.
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                          AND 1 TOPAQUINONE
                                                                                                                                                                                                                                                                                                                                           Haemosporida; Plasmodium.
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11;
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                            OXIDASE FAMILY
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RESULT 7
Q9HE41
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Best Local S
Matches 37
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Schulte U., Aign V., Hoheisel J., Brandt P., I
Schulte U., Aign V., Hoheisel J., Brandt P., I
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR 2001 (TrEMBLrel. 16, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Related to importin beta-2 subunit (Transportin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9HE41;
Q9HE41;
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Pfam; PF02786; CPSase_L_D2; 1.
Pfam; PF02787; CPSase_L_D3; 1.
Pfam; PF00117; GATase; 1.
                                                                          InterPro; PROSITE; |
                                                                                                         German Neurospora genome pre
Submitted (NOV-2001) to the
EMBL; AL451014; CAC18173.2;
HSSP; Q92973; 10BK
                                                                                                                                                                                                                                                                                                                                                                                    Related to importin B9B15.030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS: PR00096; GATASE.
PROSITE; PS01164; COPPER_AMINE_OXID_1;
PROSITE; PS00867; CPSASE_2; 1.
Copper; Oxidoreductase; TPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR005483; CPase_L.
InterPro; IPR005479; CPase_L_D2.
InterPro; IPR005480; CPase_L_D3.
InterPro; IPR005481; CPase_L_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001317; CPS_GATas; InterPro; IPR000269; CuNH_oxid. InterPro; IPR000991; GATase_1.
                                                       SEQUENCE
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID-5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1368 DNCYSSYSI 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                      2973; 1QBK.
; IPR001494; Importinb_N.
; S50166; IMPORTIN_B_NT; 1
PS50166; IMPORTIN_B_NT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR00098; CPSASE.
PR00099; CPSGATASE.
                                                     PS50166;
944 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNNRMISKNNNNLINSYNDDNKSDCFSELSYIQNHKKNINDIENDY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------VIAYSDDN-----CDVIYVPGTDGN----EEGYELWTTDYDNIPANC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNDNKSEVIKSSKNFANSTNSKCEYINSNKEKAKKINYNDENTMVYNTNEQEENENKSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEDEKS--IQAEFLEMNNADINMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEDEENNVNPD--KSMRMDDNRGNINNIANNSYYI-----RDSVYNNEYK-INKMRELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADEAANGAHQDAWKSLKAD------VENVYYMVKATYKNDPVWGNDFTCVGVMANDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNKFNEYAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1449 1449
1449 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167415 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CuNH_oxidase.
                                                                                                                                             the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _GATase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Mismatches
Score 92.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 96.5;
                                                       BSC48DCAE470DSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC72C27C72077F6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ⋛
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                        Fartmann
                                                                                                                                                 databases
                                                                                                                                                                                                                     databases
                                                                                                                                                                                                                                                                                                                                                    Sordariomycetes
                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                        В.,
                                                                                                                                                                                                                                                            Holland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GYEDLYSGS 1367
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RESULT
Q819T9
ID 9T9
ID 9T9
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DT 01
DT 01
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Best Local S
Matches 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q819T9
Q819T9;
Q1-MAR-2003
Q1-MAR-2003
Q1-MAR-2003
   Das S., Ba
Fikrig E.;
"Salp25D,
                                                                                                                                                  Ixodes scapularis (Black-legged tick) (Deer tick). Eukaryota; Metazoa; Arthropoda; Chelicerata; Arach Parasitiformes; Ixodida; Ixodidae; Ixodes. NCBI_TaxID-6945;
                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ornithodoros savignyi.
Eukaryota; Metazoa; Arthr
Parasitiformes; Ixodida;
                                                                                                                                                                                                                                                                                                                                                                                                                                Q95W25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q95WZ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FACE TO SERVICE SAIL 
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    Histamine binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of putative proteins tick salivary glands,"; Electrophoresis 22:1739-1746(2001). EMBL; AF452891; AAN76831.1; SEQUENCE 176 AA; 19375 MW; 44B755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=69826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSGP4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                           Banerjee G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCNILQMKTSPFPGK------CELWAPEGKAKNVESSCSGKFKELCGDAVETPYAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCDVIYV----PGTDGNEEGYELWTTD--YDNIPANCLNKFNE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAEFLFMNNADTNMQFA-----TEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDD- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFA-HAAN----DVWNVLKGS-DSKFLMVKRTYER-----GANKCVYMKRTSMDESSHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDEKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDV----IYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRD----VFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EV-LMGYSKAGTTTDFVEPSKYTVTATSEGASTYNMMTVRRGPASHGVKFE--LVYSDDQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDLEDGEIDDSESEGDENPDEKWT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DWADEAAN-----GAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDR-----EEDIKPQFAKKKLTRAA----NGNTAADMAKNGNAFEKVASMEEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEKSIQAEFLEMNNADTIMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLATEAAEFWLTVGEHDNLWRALEPYITDIIPVLLECMVYSP---EDIAILGGASDDEDE
      an
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3 (TrEMBLrel.
3 (TrEMBLrel.
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      Ixodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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      scapularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arthropoda; Chei
iida; Argasidae;
                                                                 DePonte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 92; DB 5;
Pred. No. 1.9;
3; Mismatches
                                                              ×.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44B7559F3BCB6A25
   antioxidant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chelicerata; Arachnida; dae; Ornithodoros.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                              Marcantonio N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67;
                                                                                                                                                                                                                Arachnida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neitz A.W.;
in granule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                              Kantor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                 E.S.
                                                                                                                                                                                                                Acari;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acari;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -YAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
RESULT 11
Q9GEV3
ID Q9GEV
AC Q9GEV
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Q9GEV3;
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EMBL; AP003185; BAB79822.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 386 AA; 44316 MW; F06209C2465839D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamas Shima T., Ogasawara N., Hattori M., Kuhara S., Hayash "Complete genome sequence of Clostridium perfringens, flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11792842;
Shimin: T
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Bacteria; Firmicutes; Clostridia;
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01-MAR-2002 (TrEMBLrel. 20, L
01-OCT-2002 (TrEMBLrel. 22, L
Hypothetical protein CPE0116.
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J. Infect. Dis. 184:0-0(2001).
EMBL; AF209913; AR807816.1; -.
SEQUENCE 221 AA; 25359 MW; 7B995AC9COAFA252 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium.
NCBI_TaxID=1502;
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                                                                                                                                                                                 RNEIY 333
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Pred. No. 5.6;
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01-MAR-2001
01-OCT-2002
                                                     Submitted
EMBL; AF48
SEQUENCE
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OBMVC3;
O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative secreted histamine binding protein.
Ixodes scapularis (Black-legged tick) (Deer tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Parasitiformes; Ixodida; Ixodidae; Ixodes.

NCBI_TaxID-6945;
                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-Rhode Island; TISSUE-Salivary
Valenzuela J.G., Francischetti I.M.,
Wather T.N., Ribeiro J.M.C.;
"Exploring the Stalome of the Tick ve
scapularis.";
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Eukaryota; Viridiplantae;
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EMBL; AF213747; AAG43878.1; -...
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InterPro; IPR001750; Ox1dored_q1.
InterPro; IPR002128; Ox1dored_q1_C.
InterPro; IPR001516; Ox1dored_q1_N.
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Asteridae; Ericales; Myrsinaceae;
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AR-2001 (TIEMBLIEL. 16, Last sequence update)
CT-2002 (TIEMBLIEL. 22, Last annotation update)
dehydrogenase subunit F (Fragment).
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PF01010; oxidored_q1_C; 1.
PF00662; oxidored_q1_N; 1.
PF00663; oxidored_q1_N; 1.
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                                                                                   AF483717; AAM93639.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEGYEL----WITDYDNIPANCLNKFNEYA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- ADTIMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCDVIYVPGTDGN
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72317 MW;
                                                        34232 MW;
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21.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pimpernel).
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                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 91.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120FA9D4E50E09E5 CRC64;
                                                     B2DB09181CC4395D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
91;
                                                                                                                                                                      Vector of
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                                                                                                                                                                                                                            gland;
Pham V.M.,
  В
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                                                                                                                                                                      Lyme
                                                                                                                 databases
Length 306;
                                                        CRC64;
                                                                                                                                                                                                                               Garfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 640;
                                                                                                                                                                      Disease,
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sequences
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RESULT 14
Q813G1
ID 0813G
AC 0813G
AC 01.M2
DT 01.M2
DT 01.M2
DT 01.M2
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Q9PQ49
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Best Local S
Matches 37
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                                                                                                                                                 O813G1 PRELIMINARY;
O813G1:
O1-MAR-2003 (TrEMBLrel. 2
O1-MAR-2003 (TrEMBLrel. 2
O1-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9PQ49
Q9PQ49;
01-OCT-2000
01-OCT-2000
01-MAR-2003
Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=36329; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          urealyticum.";
Nature 407:757-762(2000).
EMBL; AE002140; AAF30853.1;
InterPro; IPR000209; Peptidase_S8.
PROSITE; PS00138; SUBTILASE_SER; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Subject Proteome.
BYOTHER 150 AA; 52947 MW; 8D0BAB5D1FBA6206 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Serovar 3;
MEDLINE-20500219; Publ
Glass J.I., Lefkowitz
                                                                                                      Hypothetical PFE1535W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ureaplasma parvum (Ureaplasma urealyticum biotype Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
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witz E.J., Glass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.7%;
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                                                    Apicomplexa;
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Last annotation update)
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11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91; DB Pred. No. 7.5; Pred. No. 7.5;
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                                                                               3D7)
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                                                    Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Protein similar to yeast gast Glycophospholipid-anchored surface
glycoprotein, putative glycosidase that regulates the crosslinkin
beta-1,6-glucans in the cell wall.
SPAC19B12.02C.
                                                                                                                                         STRAIN=972h-;
Wood V., Rajadream M.A., Barrell B.G., Seeger K.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ datal
EMBL; AL390814; CAC00550.1; .
GeneDB_SPombe; SPAC19B12.02c; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., Hamphray S., Jagels K., James K.D., Johnson D., Kerhornou A., Kuights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L., Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E., Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M., Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., Tivey A., Unwin L., Whitehead S., Woodward J., Sulston J.E., Craig A., Newbold C., Barrell B.G; "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."; Nature 419:527-531(2002).
                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J., Peltvell T., Goble A., Goodhead I., Guilliam P., Goble A., Goodhead I., Guilliam P., Goble A., Goodhead I., Go
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces.
NCBI_TaxID=4896;
                                                              SEQUENCE
                                                                                               InterPro; IPR004886; GAS1. pfam: PF03198: GAS1: 1.
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Mungall K., Bowman S., Atkin R.,
Buckee C.O., Burrows C., Cherevan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A., Hall N., Bowman S., Churcher C., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 1083 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-22255708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 YVPGTDGNEEGYELWTTDYDNIPANCLNKFNEY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506 INNMFNEIKNIHSNDDKTKYKFSCEYIILSINILINKYIECNTTLYENYLEFLDLFIEKN 565
                                                                                            PF03198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 VENVYYMVKATYKNDPVWGNDFTC-----VGVMANDVNEDEKSIQAEFL-FMN----N 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 9.7%; Score 90.5; I
Similarity 23.5%; Pred. No. 25;
36; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YINGKEKNE-----GANRTNYYDKY 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACYVSKDNTEKVKIYIEKYKKKRKNCFENSYWKDIEFYNIED-----LYINDSKDVI 617
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                                                              542
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                                                           58115 MW;
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     9.6%;
  Score 89.5;
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                                                           1D243FDA5AD2EC3A CRC64;
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  DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                        databases
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Length 542;
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                                                                                                                                                                                                                                   Harris D.;
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Search completed: August 1, 2003, 12:19:59
Job time: 51.1829 secs

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          331.30

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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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             127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_41:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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HBP1_RHIAP
HBPM_RHIAP
GTF2_STRDO
GTF1_STRDO
YLM2_SCHPO
CYAG_DICDI
AMYG_ARXAD
CT99_HUMAN
FBN2_HUMAN
   XYNA_RUMFL
RPA2_DROME
CICA_PAEPP
FBN2_MOUSE
ITB4_UMAN
DHE2_PEPAS
HEX_ADE09
BGAL_STRTR
Y687_MSTDA
VG13_BPB03
VPAP_HSV6G
VPAP_HSV6G
VPAP_HSV6G
VPAP_HSV6G
VPAP_HSVA
VG13_BPB03
VFR4_MTCCA
APU_INGR
INGR.HUMAN
APU_THESA
YRR4_MYCCA
APU_EMENII
GUNG_CLOLO
YA97_MYCPN
YB97_MYCPN
TBP2_HAEIN
SPOT_SPICI
DIG1_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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077422 rhipicephal
077422 rhipicephal
077422 rhipicephal
P27470 streptococc
P11001 streptococc
099378 schizosacch
003101 dictyosteli
   09nud5
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| CYSP_PLAVN | C1BE_BACTU         | UN83_CAEEL | ABRA_PLAFC        | BGLR_ECOLI | ABRA_PLAFG        | OMPE_SALTI | PHLD_BACCE         | IRE1_RAT           | YE61_MYCTU | PSO2_YEAST         | POR2_XENLA |  |
|            | 085805 bacillus th |            | P22620 plasmodium |            | P23745 plasmodium |            | P33376 bacillus ce | Q63270 rattus norv |            | P30620 saccharomyc | -          |  |

## ALIGNMENTS

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| DISULFID 67 DISULFID 138 TURN 23 HELIX 27 HELIX 31 HELIX 36 TURN 42 STRAND 48 STRAND 57 TURN 59 STRAND 62 TURN 64 STRAND 62 STRAND 64 | EMBL; U96081; AAC63107<br>PDB; 1QFT; 19-APR-00.<br>PDB; 1QFY; 19-APR-00.<br>InterPro; IPR002970; H<br>Pfam; PF02098; His_bin<br>ProDom; PD152455; His_<br>Signal; 3D-structure.<br>SIGNAL 1 19 | This SWISS-PROT entry is copbetween the Swiss Institute the European Bioinformatics use by non-profit institute modified and this statement entities requires a license or send an email to license             | TISSUE-Salivary gland;  MEDLINE-99288454; PubMed Paesen G.C., Adams P.L., "Tick histamine-binding dimensional structure."; MOI. Cell 3:661-671(1999 -I- FUNCTION: BINDS HIST OUTCOMPETE HISTAMINE SUPPRESS INFLAMMATIO -!- SUBCELLULAR LOCATION | ! [   |
| 7 188<br>3 24<br>3 20<br>3 30<br>3 30<br>4 41<br>5 41<br>5 53<br>7 58<br>6 61<br>7 66<br>7 66   | .1; is_binding. ding; 1. binding; 1.  pinding; 1.  FEMALE-SPECIFIC HISTAMINE-BINDING 2.  | yright. It is produced through a of Bloinformatics and the EMBL Institute. There are no restrict strings as long as its content is is not removed. Usage by and fagreement (See http://www.isb-sibalsb-sib.ch). | -10360182; Harlos K., Nuttall P.A., Stuart D.I.; proteins: isolation, cloning, and three- ). PROTECTION INDICATES THAT ITS FUNCTION IN DURING BLOOD FEEDING. Secreted.  | ANDARD; PRT; 190 AA.  39, Created) 39, Last sequence update) 41, Last annotation update) plistamine-binding protein 2 pendiculatus (Brown ear tick) a; Arthropoda; Chelicerata; xxodida; Ixodidae; Rhipicepha |
|   |  | aboration<br>station -<br>s on its<br>no way<br>commercial<br>announce/   | 70<br>90  |   |

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dimensional structure.";
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-i- FUNCTION: BINDS HISTAMINE WITH A HIGH-AFFINITY.
OUTCOMPETE HISTAMINE RECEPTORS INDICATES THAT IT
SUPPRESS INFLAMMATION DURING BLOOD FEEDING.
SUPPRESS INFLAMMATION: Secreted.
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HSSP; 077421; 10FT.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Remaile-specific histamine-binding protein 1 precursor (I
Rhipicephalus appendiculatus (Brown ear tick).
Eukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida;
Eukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida;
Eukaryota, Metazoa; Ixodida; Ixodidae; Rhipicephalus.
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"Tick histamine-binding proteins: isolation, clon
dimensional structure".
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MEDLINE-99288454; PubMed=10360182;
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                    InterPro; IPR002970; His_binding.
Pfam; PF02098; His_binding; 1.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                         TISSUE=Salivary gland;
MEDLINE=99288454; PubMed=10360182;
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30-MAY-2000 (Rel. 39, Last annotation updat
                                                                                                                            EMBL; U96082; AAC63108.1;
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                                                                                                                                                                                                                                                                                                             Paesen G.C., Adams P.L., Harlos K.
"Tick histamine-binding proteins:
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BY SIMILARITY
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FEMALE-SPECIFIC
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                                              HISTAMINE-BINDING
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 CRC64;
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                                                                                                                                                                                                                      a collaboration
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Query Match Best Local

Similarity

Score 331.5; DB 1; Pred. No. 6.4e-22;

Length

200;

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Matches
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15-SEP-2003 (Rel. 42, Last annotation update)
Glucosyltransferase-I precursor (EC 2.4.1.5) (
(Sucrose-6-glucosyltransferase).
Streptococcus downei (Streptococcus sobrinus).
Bacteria; Firmicutes; Lactobacillales; Strepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23,
01-AUG-1992 (Rel. 23,
15-SEP-2003 (Rel. 42,
Transferase; Glycosyltransferase; Signal; Repeat; Signal 1 38 POTENTIAL.

CHAIN 39 1592 GLUCOSYLTRANSFERASE-I DOMAIN 39 1044 CATALYTIC (APPROXIMATI DOMAIN 1093 1592 6.5 x TANDER (APPRO)
                                                                                              InterPro; IPR002479; CW_binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 13.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                           modified and this statement is not removed, entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus sobrinus synthetase).";
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                                                                                                                                                              EMBL; D90213; BAA14241.1;
                                                                                                                                                                                                                                                                                                                                                                     Bacteriol, 173:989-996(1991).

Bacteriol, 173:989-996(1991).

FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURRACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl}(N) = D-fructose + {(1,6)-alpha-D-glucosyl}(N+1).

SUBCELLULAR LOCATION: Secreted.

DISEASE: DENTAL CARTES.

DISEASE: DENTAL CARTES.

1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH
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FORMS OF GLUCANS.

SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME SIMILARITY: Contains 16 cell wall binding repeats.

SIMILARITY: Contains 16 cell wall binding repeats.
                                                                                                                                                                                                                                                       European Bloinformatics Institute.
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                                                                                                                                                                                                                                        non-profit institutions as long
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a T., Kodama "
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        POTENTIAL.
GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE),
GLUCAN-BINDING (APPROXIMATE).
6.5 X TANDEM REPEATS.
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Best Local S
Matches 51
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                                                                                                                                                        J. Bacteriol. 169:4271-4278(1987).

J. Bacteriol. 169:4271-4278(1987).

II PUNCTION: PRODUCTION OF EXTRACELULAR GLUCANS, THAT ARE THOUGH TO PUNCTION: PRODUCTION OF EXTRACELULAR GLUCANS, THAT ARE THOUGH TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

I CATALYTIC ACTIVITY: Sucrose + ((1,6)-alpha-D-glucosyl)(N) = DETUCTOSE + ((1,6)-alpha-D-glucosyl)(N) = DETUCTOSE + ((1,6)-alpha-D-glucosyl)(N+1).

I SUBCELLULAR LOCATION: Secreted.

I SUBCELLULAR LOCATION: Secreted.

I J. LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11,
01-JUL-1989 (Rel. 11,
15-SEP-2003 (Rel. 42,
Glucosyltransferase-I
                                                                                                                                                                                                                                                                                                                                            Ferretti J.J., Gilpin M.L., Russell R.R.B.;
"Nucleotide sequence of a glucosyltransferase sobrinus MFe28.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus downei (Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTF1_STRDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRDO
                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MFE28
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
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                                                                                                 BINDING PROTEIN FROM S.MUTANS.
SIMILARITY: Contains 19 cell wall binding
                                                                                                                                FORMS OF GLUCANS.
SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES
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25.4%;
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Pred. No. 0
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BCOA66D079351ECF CRC64;
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2.4.1.5) (GTF-I) (Dextransucrase)
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Best Local
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Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hint S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomy Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                            YLM2_SCHPO STANDARD; PRT; 542 AA. 099378; P78853;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical protein C19B12.02c in chromosome SPAC19B12.02C.
                                                                                                                                                                                                                                                     STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities
or send a
                                                                                                                                                                                                                         MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW_binding_1; 16.
Pfam; PF02324; Glyco_hydro_70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M17391; AAC63063.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPDW-----ADEAANGAHQ-DAWKSLKADVENVYYMV-----KATYK-N 38
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1597
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                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21,
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A REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 91; [
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
1.25 A, 2 B, AND 5 AC REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomycetes;
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B9E86A200868798E CRC64;
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1.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Length 1597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             I precursor.
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Simmonds M., Squares R., Squares S., Stevens K.,

Ra Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Ra Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Galibert F., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,

RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

"The genome sequence of Schizosaccharomyces pombe.";

Nature 415:871-880(2002).
                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL390814; CAC00550.1; -
EMBL; D89203; BAA13864.1; -.
GeneDB_SPombe; SPAC19B12.02c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 4:363-369(1997).
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004886; Pfam; PF03198; GAS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
Tidentification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98162722; PubMed=9501991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=PR745
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                                                    157
                                                                                                           102
                                                                              58
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                                                                                                                                                                 44;
                                                                                                                                                                            Similarity
                                                                      EDEKSIQAEFLFMNNADTN-MQFATEKVTAVKMY----GYNRENAFRYETEDGQVFTDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4:363-369(1997).
AYYFDCGDDDDHVDFYGINIYEWCGDSDFVSSGYQERTEEFSNMTVPMI--FSEF
                         AY-----SDDNCDVI-----YVPGTDGNEEGYELWTTDYDNIPANCLNKFNEY 155
                                                                                                                                    AHQDAWKSLKADVENVYYMVKATYKNDPVWGNDF-----
                                                       E---
                                                                                                           AFQDAGIYVLSDLAQPY --
                                                                                                                                                                                                                      542
                                                                                                                                                                Conservative
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434
91
161
161
249
279
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484
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                                                    -VIQNNTNTNAAAFVKAAVRDVKSYIKSSGY-RQIPVGYSTNDEEVTRDPM
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542
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161
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                                                                                                                                                                           Score 89.5;
Pred. No. 1
                                                                                                           -EAISSSDPTWTVDLFSRYTEVVDSLAPYDNMLGFIAG--N
                                                                                                                                                                                                                                 TFSEIVALFSD -> SGGIAYQYF -> VV
                                                                                                                                                                                                                                                                                                                                                                                                                otein; Signal. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                       SER-RICH
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                                                                                                                                                                 Mismatches
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(GLCNAC...
(GLCNAC...
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                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outstation
                                                                                                                                                                Gaps
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DictyDb; DD04007; acgA.
InterPro; IPR00619; CHASE.
InterPro; IPR001054; G_cyclase.
Pfam; PF03924; CHASE; 1.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYAG_DICDI
Q03101;
01-JUL-1993
DOMAIN
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STRAND
HELIX
                                                                                                                                                PROSITE; PSSUBJY; CAROU, ... PROSITE; PSSUBJY; CAROUNTLATE_CYCLASES_1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as 100 as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structurally distinct and stage-specific adenylyl cyclase genes play different roles in Dictyostelium development."; Cell 69:305-315(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Adenylate cyclase, germination specific (EC 4
pyrophosphate-lyase) (Adenylyl cyclase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3D-STRUCTURE MODELING OF 387-543.
MEDLINE-98054247; PubMed-9391039;
Liu Y., Ruoho A.E., Rao V.D., Hur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pitt G.S., Milona
Devreotes P.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum
                                                                                                                  TRANSMEM
                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                       EMBL; M87278; AAA33164.1; PDB; 1AWM; 28-JAN-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Catalytic mechanism of the adenylyl and mutational analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-92233467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGA OR ACG
                                                                                                                                             D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).

C. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).

FUNCTION: ACG HAS A LARGE EXTRACELLULAR DOMAIN WHICH MAY BE INVOLVED IN THE RECOGNITION OF AN EXTRACELULAR SIGNAL PRES DURING THE CYTOPLASMIC DOMAIN.

CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.

ENZYME REGULATION: INSENSITIVE TO GUANINE NUCLEOTIDES.

SUBCELLULAR LOCATION: Type II membrane protein.

DEVELOPMENTAL STAGE: AFTER FRUITING BODIES HAVE BEEN FORMED DURING GERMINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 CHASE domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyclase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the adenylyl cyclase class-4/guanylyl
                                                                                                                                                                                                      PS50839; CHASE; 1
   42
396
738
835
403
                                                                                                                  19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=1348970;
N., Borleis J.,
                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                            EXTRACELLULAR (POTENTIAL). CHASE. GUANYLATE CYCLASE. ASN-RICH. POLY-ASN.
                                                                                                 CYTOPLASMIC (POTENTIAL) SIGNAL-ANCHOR (TYPE-II (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hurley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.H.;
and guanylyl cyclases: modeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             858
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RESULT 8
AMYG_ARXAD
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Best Local S
Matches 39
                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                          Bul Minh D., Kunze I., Foerster S., Wartmann T., Horstmann Manteuffel R., Kunze G., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-I- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked
                                                                                                                                                                                                                                                                                                                       AMYG_ARXAD STANDARD; PRT; 624 AA. P42042; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update Glucoamylase precursor (EC 3.2.1.3) (Glucan (1,4-alpha-D-glucan glucohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELIX
SEQUENCE
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STRAND
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STRAND
                                        EMBL; Z46901; CAA86997.1; -. HSSP; P04064; 1GAI.
                                                                                                                                        This
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TURN
InterPro; IPR005036; CBM_21.
InterPro; IPR000105; Glyco_hydro_15
Pfam; PF03370; CBM_21; 1.
Pfam; PF00723; Glyco_hydro_15; 1.
                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                               <del>-</del>
                                                                                                                                                                                                                                                                                 Arxula adeninivorans (Yeast).
Eukaryota; Fungi; Ascomycota; Sac
Saccharomycetales; Dipodascaceae;
                                                                                                                  between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                        STRAIN-LS3;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       NCBI_TaxID=37620;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAND
                                                                                                                                                              with release of beta-D-glucose. SIMILARITY: BELONGS TO FAMILY 15 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                  glucose residues successively
                                                                                                                             SWISS-PROT entry is copyright. It is produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SYFPILHAFPDINKDII------GLDINSTDYMNETIKKSIFNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVFTDVIAYSDDNCDVIYVPGTDGNEEGYELWTTDYDN--IPANCLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LNTTLKNSEFQYLFWIKKINNNDRNCFEEKFSKEIKDTFQIYSFDENTNSIHVAKNKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDVNEDEKSIQAEFLF----MNNADTNM----QFATEKVTAVKMYGYNRE-NAFRYETEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSEEENSNIQMDLERSSKQIIHNIQMNAMYLLSSIDTLKALYYVNPNFDRNDFNVF----
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llarity 23.2%;
Conservative :
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Pred. No. 8.6;
31; Mismatches
                                                                                                                                                                                                                                                                                 Saccharomycotina; Saccharomycetes; eae; mitosporic Dipodascaceae; Arxula.
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RP SEQUENCE FROM N.A.

RP MEDLINE-21638749; PubMed-11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,
RA Dones M., Stavrides G., Almeida J.P., Babbage A.K., Begre D.M.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burill W.D., Butler A.P., Carder C., Carter N.P.,
RA Clegy S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Clegy S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegy S., Cobley V.E., Collier R.E., Connor R.E., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kinberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehvaeslaiho M.H., Leversha M.A., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMuïray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Best I
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C100RF99.
HOmo sapiens (Human).
Homo sapiens (Human).
Thereas, Chordata,
Thereas, Primates,
                                                                                                                                                                                                                                                                                                                                                                                        Q9NUD5;
28-FEB-2003
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CARBOHYD
CARBOHYD
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ACT_SITE
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                    Hypothetical C200RF99.
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SIGNAL
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PROSITE;
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28-FEB-2003
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; PS00820;
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(Rel.
(Rel.
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111
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; GLUCOAMYLASE;
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41,
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624
340
343
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70
98
1111
168
267
233
333
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21.5%;
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CATALYTIC BASE (BY SIMILARITY).
GENERAL ACID CATALYST (BY SIMILARITY).
INTERACT WITH SUBSTRATES (BY SIMILARITY).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 84; DB
Pred. No. 6.5;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGRYPEDVY
                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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5.5;
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Homo.
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RESULT 10
FBN2_HUMAN
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Best Local
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P35556;
01-JUN-1994
01-FEB-1996
28-FEB-2003
Fibrillin 2
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ZN_FING 3
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ZN_FING 3
DOMAIN
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                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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"The DNA sequence and com Nature 414:865-871(2001).
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InterPro; IPR001878;
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E; PS50158; ZF_CCHC;
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3 (Rel. 41, Last anno
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8; ZF_CCHC; 2.
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151 CCHC-TYPE 1.

169 CCHC-TYPE 2.

170 CCHC-TYPE 3.

171 POLY-GLY.

184 POLY-ALA.

185 POLY-ALA.
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on update)
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SEQUENCE FROM N.A.
MEDLINE-94165150; PubMed-8120105;
Zhang H., Apfelroth S.D., Hu W., Davis
Bonadio J., Mecham R.P., Ramirez F.;

expression

of.

fibrillin-2,

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novel Sanguineti

microfibrillar

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a

NCBI\_TaxID=9606;

Craniata; Vo Catarrhini;

Vertebrata;

Euteleostomi;

Hominidae;

Homo

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EMBL; U03272; AAA18950.1; -.

REMBL; X62009; -; NOT_ANNOTATED_CDS.

PIR; A54105; A54105.

RESP; P35555; 1EMN.

RESP; P35555; 1EMN.

REGENEW; HGNC:3604; FBN2.

REGO; GO:0005578; C:extracellular matrix; TAS.

REGO; GO:0005271; F:extracellular matrix structural constituent; TAS.

REGO; GO:00052745; P:embryogenesis and morphogenesis; TAS.

REGO; GO:0007345; P:embryogenesis and organogenesis; TAS.

REGO; GO:0007397; P:histogenesis and organogenesis; TAS.

REGO; GO:0007345; P:embryogenesis and organogenesis; TAS.

REGO; GO:0007345; P:embryogenesis and organogenesis; TAS.

REGO; GO:0007345; P:histogenesis and organogenesis; TAS.

REGO; GO:0007345; P:histogenesis and organogenesis; TAS.

REGO; GO:0007345; P:histogenesis and organogenesis; TAS.

REGO; GO:0007345; P:his
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WARIANTS CCA TYR-1252 AND SER-143032;

WARIANTS CA TYR-1259; PubMed-7493032;

Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.;

"Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder,

"Congenital contractural arachnodactyly.";

"L Nat. Genet. 11:456-458(1995).

"A National Contractural arachnodactyly.";

"A PVARIANTS CCA HIS-1114.

"MEDLINE-98407789; PubMed-9737771;

"A Babcock D., Gasner C., Francke U., Maslen C.;

"A single mutation that results in an asp-to-his substitution and

"T Partial exon skipping in a family with congenital contractual

"T arachnodactyly.";

"A single mutation that results in an asp-to-his substitution and

"T Partial exon skipping in a family with congenital contractual

"T A single mutation that results in an asp-to-his substitution and

"T Partial exon skipping in a family with congenital contractual

"T Partial Exon Skipping in a family with congenital contractural

"T PARTIANTS CCA PHE-1141 AND TRP-1252.

"MEDLINE-20259236; PubMed-10797416;

"MEDLINE-20259236; PubMed-10797416;

"MEDLINE-20259236; PubMed-10797416;

"MEDLINE-20259236; PubMed-10797416;

"MEDLINE-20259236; PubMed-10797416;

"MEDLINE-20259236; PubMed-10797416;

"MEDLINE-30259236; PubMed-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.ch).
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Nature
[3]
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11. FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFI FUNCTION: STRUCTURAL COMPONENT OF CONTAINING MICROFIBRILS REGINAL PROBLEM FOR THE PROBLEM FOR ELASTIC FIBER ASSEMBLY.

11. DISEASE: DEFECTS IN FBN2 ARE THE CAUSE OF CONCENITAL CONTRA ARACHNODACTYLY (CCA) (ALSO KNOWN AS BEALS SYNDROME). CCA IS PHENOTYPICALLY SIMILAR TO MARRAN SYNDROME, BUT DOES NOT EFF AGRIA AND THE EYES.

11. SIMILARITY: Contains 47 EGF-like domains.

12. SIMILARITY: Contains 47 TGF-beta binding protein (TGFBP) dom THE BEALS (Fiber Homepage; NOTE-FIbrillin 2 pag WWW-"http://ef.wustl.edu/genes/FBN2.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           component preferentially located J. Cell Biol. 124:855-863(1994).
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Am. J. Med. Genet
-1- FUNCTION: STF
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PROSITE; PS01186;
PROSITE; PS01187;
Extracellular matr
     REGPEAT; SIGNAIN
CHAIN
DOMAIN

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                                                                                                                                                                                                                                                                                                022; EGF_1; 2.
186; EGF_2; 37.
187; EGF_CA; 42.
matrix; Calcium-binding;
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        ; 2.
37.
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     FUBRILLIN I EGGF-LIKE 2 2 EGGF-LIKE 1 1 EGGF-LIKE 2 2 EGGF-LIKE 1 EGGF-LIKE 1 EGGF-LIKE 2 2 EGGF-LIKE 3 EGGF-LIKE 2 EGGF-LIKE 2 EGGF-LIKE 3 EGGF-LIKE 3 EGGF-LIKE 4 EGGF-LIKE 4 EGGF-LIKE 5 EGGF-LIKE 5 EGGF-LIKE 5 EGGF-LIKE 6 EGGF-LIKE 6 EGGF-LIKE 6 EGGF-LIKE 7 EGGF-LIKE 7 EGGF-LIKE 8 EGGF-LIKE 
     GGF-LIKE 41, CFGF-LIKE 42, CFGF-LIKE 43, CFGF-LIKE 44, CFGF-LIKE 46, CFGF-LIKE 47, CFGF-LIKE 47, CFGF-LIKE 47, CFGF-LIKE 47, CFGF-LIKE 47, CFGF-LIKE 47, CFGGF-LIKE 47, CFGF-LIKE 47, CFGGF-LIKE 47, CFGF-LIKE 4
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Matches · 45
                                                                           XYNA_RUMFL
P29126;
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28-FEB-2003
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  MEDLINE=92261318; PubMed=1584021; Zhang J.-X., Flint H.J.;
                                   Ruminococcus.
NCBI_TaxID=1265;
                STRAIN=17
                      SEQUENCE FROM N.A.
                                                  Bacteria;
                                                       Ruminococcus flavefaciens
                                                                XYNA.
                                                                      Bifunctional
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49; Conserv
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                                                                                                                                                                          QAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFT----DVIAYSD-DNC
                                                                                                                                                     DV--IYVPGTDGN----
                                                                                                                                                                                            DECSNGTHQ---CSINAQCVN----TPGSYRCACSEGFTGDGFTC----
                                                                                                                                                                                                     DEAANGAHQDAWKSLKADVENVYYMVKATYK---NDPVWGNDFTCVGVMANDVNEDEKSI
                                                  Firmicutes;
                                                                   (Rel. 24, Created)
(Rel. 24, Last sequence update)
(Rel. 41, Last annotation update)
l endo-1,4-beta-xylanase XYLA prec
                                                                                                                                                                                                                        Conservative
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                                                                                                       STANDARD;
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                                                 Clostridia;
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Pred. No. 44;
l6; Mismatches
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                                                Clostridiales;
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                                                                    precursor
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                                                Lachnospiraceae
                                                                                                                                                                                                                                    Length 2911;
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(Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 38, Last annotation updat
(Rel. 38 polymerase I 135 kDa polyp
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InterPro; IPRO01100; Glyco_hydro_10.
InterPro; IPR001137; Glyco_hydro_11.
pfam; pF00331; Glyco_hydro_10; 1.
pfam; pF00457; Glyco_hydro_11; 1.
prints; pR00134; GLHYDRLASE10.
pRINTS; pR00911; GLHYDRLASE11.
SMART; SM00911; GLHYDRLASE11.
SMART; SM00633; Glyco_10; 1.
pROSITE; pS00571; GLYCOSYL_HYDROL_F10; 1.
pROSITE; pS00776; GLYCOSYL_HYDROL_F11_1; 1.
pROSITE; pS00777; GLYCOSYL_HYDROL_F11_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (see or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linkages in xylans.
-!- PARHWAY: Xylan degradation.
-!- SIMILARITY: IN THE N-TERMINAL SECTION;
G (FAMILY 11 OF GLYCOSYL HYDROLASES).
-!- SIMILARITY: IN THE C-TERMINAL SECTION;
F (FAMILY 10 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z11127; CAA77476.1;
PIR; S20907; S20907.
HSSP; P48793; 1XND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A bifunctional xylanase encoded by the xynA gene of the incellulolytic bacterium Ruminococcus flavefaciens 17 compridissimilar domains linked by an asparagine/glutamine-rich Mol. Microbiol. 6:1013-1023(1992).

-!- FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XYLO-OLIGOSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xylan degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND DOMAIN 2 MORE XYLOSE.
-I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                              SDDNCDVIYVPGTDGNEEGYELWTTDYDNIPANC---LNKFNEYAVGRETRDVFTSA
                                                                                                                                                                                                          NEDEKSIQAEFLFMNNADTNMQFATEKVTAVKMYGYNR--ENAFRYETEDGQVFTDVIAY 114
                                                                                                                                                                                                                                                                      PDWFFRENFSQNGAYVSKDIMNQRLESMIKNTFAALKSQYPNLDVYSYD-VC-
                                                                                                                                                                                                                                                                                                           PDW----ADEAANGAH--QDAW-KSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDV
                                                                                                                                                                                                                                                                                                                                                         Conservative
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                          8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR 28, OR 29 (POTENTIAL).
BIFUNCTIONAL ENDO-1,4-BETA-XYI
XYLANASE DOMAIN 1.
ASSU/GLN/TRP-RICH (LINKER).
XYLANASE DOMAIN 2.
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is not removed.
                                                                                                                                                                                                                                                                                                                                                                          Score 82.5;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTON DONOR (BY SIMILARITY)
PROTON DONOR (BY SIMILARITY)
NUCLEOPHILE (BY SIMILARITY).
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1033567D4B526EBD CRC64;
1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                      -PAGCKLYLNDYNEY-IPAKTNDIYNMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multifunctional enzyme;
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e-rich sequence.
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KONTERMANN R., Sitzler S., Selfarth W., Petersen G., Bautz E.K.F.;
"Primary structure and functional aspects of the gene coding for the second-largest subunit of RNA polymerase III of Drosophila.";
MOI. Gen. Genet. 219:373-380(1989).
-1- FUNCTION: DNA DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES. RNA POLYMERASE I IS ESSENTIALLY USED TO TRANSCRIBE
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF04563; RNA_pol_Rpb2_2; 1.
Pfam; PF04565; RNA_pol_Rpb2_2; 1.
Pfam; PF04565; RNA_pol_Rpb2_5; 1.
Pfam; PF04567; RNA_pol_Rpb2_5; 1.
Pfam; PF04560; RNA_pol_Rpb2_6; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; J00354; J00354.
FlyBase; FBgn0003278; RPI135.
InterPro; IPR001572; RNA_DOL_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     Transferase; DNA-directed RNA polymerase; Transcription; Zinc; Zinc-finger; Nuclear protein.
ZN_FING 1061 1093 C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KNA polymerase I subunit RPI135.
                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01166; RNA_POL_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
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SIMILARITY: Belongs to the RNA polymerase beta chain family.
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MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA
FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE
PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: EACH CLASS OF RNA POLYMERASE IS DIFFERENT POLYPEPTIDES. THIS SUBUNIT IS COMPONENT OF RNA POLYMERASE I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIBOSOMAL DNA UNITS.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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                                                                                                                               218
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                                                                                                                                                                                                                           11
                                                                                                                                                             8
                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                         HGEHDSEWGGIFVIRGNEKIVRMLIMTRRNHPICVKRSSWKDRGQNFSDLGMLVQTVRED
                                                                                                                              ESSLSNVVHYLNNGTAKFMFSHVK
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1129 AA;
 (Rel. 40, Created)
(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                          Conservative
                                                STANDARD;
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                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                        Score 81.5;
Pred. No. 22;
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W; E0A15FF1BCEF18D7
                                                PRT;
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                                                                                                                                                                                                                                                                                     Length 1129;
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RESULT
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Best Local
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Q61555; Q63957;
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
28-FEB-2003 (Rel. 4
Fibrillin 2 precurs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patel R., Yousten A.A., Rippere K.;

"Detection of two new cry genes in Paenibacillus popilliae.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB

LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE

CELLS OF P.POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).

CELLS OF P.POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).

OF THE SPORUCATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

OF THE SPORE COAT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Paenibacillus popilliae (Bacillus Paenibacillus popilliae)
                                                                                                                                                                                                                                                                                                                         MOUSE
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InterPro;
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Parasporal crystal protein cryl8Ca (Parasporal
CryXVIIC(a)) (Crystaline parasporal protoxin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03944; endotoxin_C;
Pfam; PF03945; endotoxin_N;
                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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EMBL; L39790; AAA74908.1; -.
EMBL; S69359; AAC60685.1; -.
PIR; A57278; A57278.
HSSP; P35555; IEMN

G0; G0:0030326; P:limb morphogenesis; IMP.
InterPro; IPR001152; Asx_hydroxyl.
InterPro; IPR001212; Fibril-assoc.
InterPro; IPR002212; Fibril-assoc.
Pfam; PF00008; EGF; 45.
InterPro; IPR001210; EGFELOD.
SMART; SM00179; EGF_CA; 43.
PROSITE; PS00010; ASX_HYDROXYL; 43.
PROSITE; PS01186; EGF_1; 2.
PROSITE; PS01187; EGF_CA; 43.
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MEDLINE-95263670; PubMed-7
Zhang H., Hu W., Ramirez F
"Developmental expression of extracellular microfibr.
J. Cell Biol. 129:1165-117([2])
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Genomics
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MEDLINE-94140368; PubMed-8307578;
Li X., Pereira L., Zhang H., Sanguineti
Francke U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      brillin genes map to regions of conserved mouse/human synteny on see chromosomes 2 and 18.";
see chromosomes 2 and 18.";
omics 18.667-672(1993).
FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
SIMILARITY: Contains 47 EGF-11ke domains.
SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBI outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in by non-profit institutions are no usage by and for content is the state of 
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      Family.

POTENTIAL.

FIBRILIN :

EGF-LIKE 1

EGF-LIKE 3

EGF-LIKE 4

EGF-LIKE 5

EGF-LIKE 6

EGF-LIKE 7

EGF-LIKE 9

EGF-LIKE 1

EGF-LIKE 11

EGF-LIKE 12

EGF-LIKE 11

EGF-LIKE 11
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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Integrin beta-4 precursor (GP150) (CD104 antigen).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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"A novel integrin (al.

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EMBO J. 8:672
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SEQUENCE FROM N.A. (ISOFORM MEDLINE-90183973; PubMed-23 SUZUKÍ S., Naitoh Y.;
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[6]
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MEDLINE-97311186;
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MEDLINE=21149723; PubMed=11251584;
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mutations
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pan. J. Pathol. 152:157-166(1998).
                                                                                                                                                             Stevens
                                                                                                                                                                           Nakano A., Pulkkinen L., Murrell D.,
                                                                                                                                                                                                                                                                                                                                                      Hirano
                                                                                                                                                                                                                                                                                                                                                                      VARIANTS HIS-98 A
MEDLINE-21183353;
                                                                                                                                                                                                                                                                                           (ITGB4)
                                                                                                                                                                                                                                                                                                                                                                                                                                               bullosa with
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MEDLINE-20255363; Pubr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Br. J.
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                                                                                                                                       "Epidermolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Alpha 6 beta 4 integrin abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A homozygous missense mutation in the cytoplasmic
integrin, G931D, that disrupts hemidesmosome assemi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inoue M., Tamai K., McGrath J.A.;
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MEDLINE=98206430; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the integrin beta4 gene (ITGB4) in ld disease.";
iatr. Res. 49:618-626(2001).
FUNCTION: INTEGRIN ALPHA-6/BETA-4
PLAYS A CRITICAL STRUCTURAL ROLE 1
EPITHELIAL CELLS.
SUBUNIT: HETERODIMER OF AN ALPHA F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Invest.
                                                                                                                                                                                                                                                                     novel single-nucleotide polymorphisms.
4) gene in the Japanese population.";
m. Genet. 46:35-37(2001).
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                                                                                                                                                             C.A.,
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L., Bruckner-Tuderman L., August C.,
heterozygosity for missense (L156P)
in the beta-4 integrin gene (ITGB4)
phenotype of epidermolysis bullosa w
thol. 152:935-941(1998).
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ol. 144:408-414(2001).
                                                                                                                  lkkinen L., Murrell D., Rico J., Luc) Robertson S., Pfendmer E., Uitto J., s bullosa with congenital pyloric at the beta 4 integrin gene (ITGB4) and
                                                                                                                                                                                                                                                                                                                                                                      AND LEU-844.
3; Pubmed=11289717;
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l epidermolysis bullosa
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pyloric atro
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-!- DOMAIN: THE FIBRONECTIN TYPE III-LIKE DOMAINS BIND BPAGI AND PLECTIN AND PROBABLY ALSO RECRUIT BP230-
-!- DISEASE: DEFECTS IN ITGB4 ARE A CAUSE OF EPIDERMOLYSIS BULLOSA LETALIS WITH PYLORIC ATRESIA (EB-PA), ALSO KNOWN AS JUNCTIONAL EPIDERMOLYSIS BULLOSA WITH PYLORIC ATRESIA (PA-JEB) OR APLASIA CUTIS CONGENITA WITH GASTROINTESTINAL ATRESIA. IT IS CHARACTERIZED BY MUCCUTNAMOUS FRAGILITY AND GASTROINTESTINAL ATRESIA, WHICH MOST COMMONLY AFFECTS THE PYLORUS.
-!- DISEASS: DEFECTS IN ITGB4 ARE A CAUSE OF GENERALIZED ATROPHIC BENIGN EPIDERMOLYSIS BULLOSA (GABEB). THIS NONLETHAL FORM OF JUNCTIONAL EPIDERMOLYSIS BULLOSA (GABEB) CHARACTERIZED BY LIFE-LONG BELISTERING OF THE SKIN, ASSOCIATED WITH HAIR AND TOOTH
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SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN SIMILARITY: Contains 4 fibronectin type III dom SIMILARITY: Contains 2 WWFA-like domains.

CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN TO 1429 DUE TO A FRAMESHIFT.

DATABASE: NAME-PROW; NOTE-CD guide CD104 entry;
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                                                                                                                                                                                                                                                            non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.lsb-sib.ch/announce/
                                                                                                                                  WPNSDPPFSFKNVISLTEDVDEFRNKLQGERISGNLDAPEGGFDAILQTAVCTRDIGWRP
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ASSOCIATES WITH ALPHA-6

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         PIR_76:*
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pir2:*
pir3:*
pir4:*
         T18282
AC1582
AC1583
AB1347
AA42239
A54105
S57962
S57962
S20907
JQ033
T51637
T51637
E84717
A1715
A1717
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H82891
H97012
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integrin beta-4 pr
integrin beta-4 ch
L-lactate dehydrog
hypothetical prote
hypothetical prote
hypothetical prote
prophage pi3 prote
glutamate dehydrog
hexon protein - hu
                                                                                                                                                                                                                                                                                                                             probable peptidogladenylate cyclase fibrillin-2 precur cspC protein - Clo endo-1,4-beta-xyla DNA-directed RNA pmyb-related transc probable MYB famil hypothetical prote hypothetical prote fibrillin-2 precur branched-chain alp vitellogenin - Ather (Somal Washer)
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hypothetical prote
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integrin beta-4 pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glucosyltransferase precursor - Streptococcus sobrinus
(;Species: Streptococcus sobrinus
(;Species: Streptococcus sobrinus
(;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 15-Oct-1999
(;Accession: A38175
R;Abo, H.; Mtsumura, T.; Kodama, T.; Ohta, H.; Fukui, K.; Kato, K.; Kagawa, H.
J. Bacteriol. 173, 989-996, 1991
A;Title: Peptide sequences for sucrose splitting and glucan binding within Streptococ
A;Reference number: A38175; MUID:91123227; PMID:1704006
A;Accession: A38175
A;Saccession: A38175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
A38175
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| hypothetical prote | H72455 | N        | 515  | 8.1     | 76   | ັດ |
|--------------------|--------|----------|------|---------|------|----|
| nitrate reductase  | G72603 | N        | 466  | 8.1     | 76   | 4  |
| DNA polymerase pro | T09322 | N        | 403  | 8.1     | 76   | ω  |
| early nuclear anti | QQBEHG | <b>—</b> | 368  | 8.1     | 76   | ถ  |
| reverse transcript | T06182 | ຎ        | 153  | 8.1     | 76   | Ξ  |
| probable helicase  | H84464 | N        | 1219 | 8.2     | 76.5 | 5  |
| hypothetical prote | E71610 | N        | 669  | 8.2     | 76.5 | 6  |
| toxin-like outer m | A64556 | N        | 2893 | 8.2     | 77   | æ  |
| hypothetical prote | S06256 | N        | 393  | 8.2     | 77   | 37 |
| uncharacterized co | F97343 | N        | 366  | 8.2     | 77   | õ  |
| hypothetical prote | G64385 | N        | 335  | 8.2     | 77   | 5  |
| hypothetical prote | E89769 | N        | 256  | 8.2     | 77   | 4  |
| hypothetical prote | A59103 | N        | 150  | 8.2     | 77   | ພ  |
| endo-beta-N-acetyl | G95057 | Ŋ        | 1659 | 8.3     | 77.5 | ຄ  |
| hypothetical prote | н97926 | N        | 1659 | 8       | 77.5 | ĩ  |
| beta-galactosidase | A49750 | ພ        | 1026 | 8<br>.3 | 77.5 | 30 |

## ALIGNMENTS

|  |   | <br><del> </del> | <br>  | <br> |     |  |
|--|---|------------------|---|------|-----|--|
| A Cross references GB:D90213; NID:g217032; PIDN:BAA14241.1; PID:d1014946; PID:g21703 C:Superfamily: cpl repeat homology <cpl>F:1093-1127/Domain: cpl repeat homology <cpl>F:122-1241/Domain: cpl repeat homology <cpl>F:122-1241/Domain: cpl repeat homology <cpl>F:1320-1151/Domain: cpl repeat homology <cpl>F:1330-1151/Domain: cpl repeat homology <cpl>F:1330-1151/Domain: cpl repeat homology <cpl>F:1465-1484/Domain: cpl repeat homology <cpl>F:1465-1484/Domain: cpl repeat homology <cpl>F:1465-1484/Domain: cpl repeat homology <cpl>F:1510-1153/Domain: cpl repeat homology <cpl>F:1465-1484/Domain: cpl repeat homology <cpl>F:1510-1153/Domain: cpl repeat ho</cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl></cpl> | A; Residues: 1-1592 (ABO)  A; Residues: 1-1592 (ABO)  A; Cross-references: GB:D90213; NID:g217032; PIDN:BAA14241.1; PID:d1014946; PID:g21703  C; Superfamily: cpl repeat homology (CP1)  F;1093-1112/Domain: cpl repeat homology (CP2)  F;122-1241/Domain: cpl repeat homology (CP3)  F;1330-1351/Domain: cpl repeat homology (CP5)  F;1330-1371/Domain: cpl repeat homology (CP5)  F;1402-1420/Domain: cpl repeat homology (CP5)  F;1402-1420/Domain: cpl repeat homology (CP6)  F;1413-1532/Domain: cpl repeat homology (CP6)  F;1451-1532/Domain: cpl repeat homology (CP8)  Query Match  Best Local Similarity 25.4%; Pred. No. 0.52;  Matches 51; Conservative 19; Mismatches 55; Indels 76; Gaps 12;  Oy  2 OPDWADEAANGAHO-DAWKSLKADVENVYMV |                  | 395 DPLGGYDFLLANDVDNSNPVVQAEQLNWLHYLLNFGSIYANDADANF | 442  | 139 | RESULT 2 H82891 hypothetical protein UU441 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: H82891 |

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RESULT 4
T18282
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A; Cross-references: GB: AE001437; PIDN: AAK78891.1; A; Cross-references: GB: AE001437; PIDN: AAK78891.1; A; Cross-references: Clostridium acetobutylicum
   R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, K.J.; Kiyosawa, Genetics 148, 1117–1125, 1998
A;Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to t
                                                   C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T18.882; S2.8718
                                                                                            hypothetical protein G6 - slime mold (Dictyostelium discoideum) C; Species: Dictyostelium discoideum
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H97012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: R; Nolling, J
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A;Residues: 1-450 <GLA>
A;Cross-references: GB:AE002140; GB:AF222894; NID:g6899420;
A;Experimental source: serovar 3; biovar 1
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A;Description: The complete sequence
A;Reference number: A82870
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27; Conserv
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37; Conserv
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                                                                                                                                                                                                                                     SDDNCDVIYVPGTDGNEEGYELWTTDYD-----NIPANCLNKFNE
                                                                                                                                                                                                                                                                        DTNAEKQAI-SPYIY----GTNQDFSNAKVTA-RRIGGNRSTGYNWENNDSNA----
                                                                                                                                                                                                                                                                                                          DVNEDEKSIQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAY 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVG----VMANDVNEDEKS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 91; DB Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                            Score 88; DB 2; Length 606; Pred. No. 5;
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A; Residues: 1-1237 <GLA>
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science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A;Title: Comparative genomics of Listeria species, A;Reference number: ABI077; MUID:21537279; PMID:11679669
A;Accession: AC1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: AC1583
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.;
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duss
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A;Residues: 37-254 <GUR>
A;Cross-references: EMBL:X53237; NID:g7280; PIDN:CAA37327.1;
A;Experimental source: plasmid Ddpl
                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AL592022; PIDN:CAC96435.1; A;Experimental source: strain Clip11262
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A;Accession: T18282
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internalin protein (LPXTG motif) homolog lin1204 [imported] - Listeria innocua
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848 MPSNAQGEFSLEEQTVTYIYSKNPVPAKDITVQYTDEDGMELAPTETLS-GNVDENYVT-
                                                                                                   788 IKATPKEVIVYIDAVQGANITVKYEDESGNKLAENSILTGNVGEEYSSSAKEILGYTLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 ENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDEKSIQAEFLFMNNADTNMQFATEKVT
                                             ADTIMQ--FATEKVTAVKMYGYN----RENAFRYETEDGQVFTDVIAYSDDNCDVIYVPG
                                                                                                                                                 LKADVENVYYMVKA-----TYKNDPVWGNDFTCVGVMANDVNEDEKSIQAEFL--FMNN
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Pred. No. 21;
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surget, O.;
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P :
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Voss, H.; Wehla
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A; Delcule type: DNA
A; Molecule type: DNA
A; Residues: 1-1612 <GLA>
A; Cross-references: GB:NC_003210; PIDN:CAD00256.1; PID:g16411648; GSPDB:GN00177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazqu A; Title: Comparative genomics of Listeria species. A; Reference number: AB1077; MUID:21537279; PMID:11679; A; Accession: AB1347
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                                                                                                                                                                                       C; Superfamily: sl.
C; Keywords: phospi
F; 351-574/Domain:
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C;Superfamily: slime mold germination stage adenylate
C;Keywords: phosphorus-oxygen lyase
                                                                                                                                                                                                                                                                                                        R;Pitt, G.S.; Milona, N.; Borleis, J.; Lin, K.C.; Reed, R.R.; Devreotes, Cell 69, 305-315, 1992
A;Title: Structurally distinct and stage-specific adenylyl cyclase genes A;Reference number: A42239; MUID:92233467; PMID:1348970
A;Accession: A42239
                                                                                                                                                                                                                                                                                                                                                                                             adenylate cyclase (EC 4.6.1.1) germination stage - slime mold (Dictyostelium C;Species: Dictyostelium discoideum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A42239
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R;Glaser, P.; Frange
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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AB1347
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                                                                                                                                                                                                                                                             A; Residues: 1-858 <PIT>
                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid
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Best Local
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Dominguez-Bernal, G.; Duc
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                                                                                                                                        Similarity
NDVNEDEKSIQAEELF----MNNADTNM----QFATEKVTAVKMYGYNRE-NAFRYETEDG
                                                                       WADEAANGAHQDAWKSLKADVENV----YYM-----VKATYKNDPVWG-NDFTCVGVMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SIQAEFL-----FMNNADTNMQFATEKVTA----VKMYGYNRENAFRYETEDGQVF
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23.2%; Pred. No. 16;
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Pred. No. 29;
22; Mismatches
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Vazquez-Boland, J.A.;
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                                                                                                                                                       Length 858;
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Voss, H.; W
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K.D.; 1
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Fsihi, H.
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                                              cspC protein - Clostridium acetobutylicum (fragment)
C;Species: Clostridium acetobutylicum
C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #
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C; Accession: S57962
R; Sanchez-Beato, A.
submitted to the EM
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A; Residues: 1-2918 <ZHA>
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Best Local :
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                 Garcia,
Data
Library,
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RiMilewicz, D.M.
RiMilewicz, D.M.
Submitted to the EMBL Data Library,
Submitted to the EMBL Data Library,
Submitted to the EMBL Data Library,
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R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattel, M.(
Nature 352, 330-334, 1991
A;Title: Linkage of Marfan syndrome and a phenotypically
A;Reference number: S17062; MUID:91304567; PMID:1852206
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                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-29/Domain: signal sequence #status predicted F;30-2918/Product: fibrillin-2 #status predicted F;1245-1280/Domain: EGF homology <EGF1>F;1970-2013/Domain: EGF homology <EGF>.
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A;Residues: 752-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928
A;Cross-references: EMBL:X62009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: extracellular protein
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A; Residues: 752-1407, 'R', 1409-1489, 1791, 'GS', 1794-1796, 'QLI', 1922-1923, 'LD', 1926, 'P',
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                                                                                                                                                                                                                     DECSNGTHQ---CSINAQCVN----TPGSYRCACSEGFTGDGFTC-----SDVDECAENI 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVFTDVIAYSDDNCDVIYVPGTDGNEEGYELWTTDYDN--IPANCLNK
SFONICVSGTCNNLPGMFHCICDDGYELDRTGGNCTDIDECADPINCVN
                                                   DV--IYVPGTDGN----
                                                                                                                                                              QAEFLEMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFT---DVIAYSD-DNC 119
                                                                                                                                                                                                                                                                           DEAANGAHQDAWKSLKADVENVYYMVKATYK---NDPVWGNDFTCVGVMANDVNEDEKSI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- LNTTLKNSEFQYLFWIKKINNNDRNCFEEKFSKEIKDTFQIYSFDENTNSIHVAKNKS
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                      8.9%;
                                                                                                                                                                                                                                                                                                                               16;
                                                ----EEGYEL-----WTTDYDNI--PANCLN 150
                                                                                                                                                                                                                                                                                                                                                      Score 83.5;
Pred. No. 95;
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                                                                                                          -LNVPGAYRCECEMG - - FTPASDSRSCQDIDEC
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                                                                                                                                                                                                                                                                                                                                                                                      BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shown;
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                                                                                                                                                                                                                                                                                                                          Gaps
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$20907
endo-1.4-beta-xylanase (EC 3.2.1.8) precursor, endo-1.4-beta-xylanase (EC 3.2.1.8)
                                                                                                                                                                                                                                                                                                                      F;249-622/Domain: linker region B #status predicted <LRB>
F;623-954/Domain: catalytic domain C #status predicted <CDC>
F;655-953/Domain: Streptomyces endo-1,4-beta-xylanase A homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Date: 22-No
C; Accession:
                                                                                                                                                                                                                                                                                                                                                             F;249-622/Domain: linker region B
                                                                                                                                                                                                                                                                                                                                                                               F;1-27/Domain: signal sequence #status predicted <SIG>F;28-954/Product: bifunctional endo-1,4-beta-xylanase #status F;28-954/Product: bifunctional n #status predicted <CDA>F;28-248/Domain: catalytic domain A #status predicted <CDA>F;40-236/Domain: endo-1,4-beta-xylanase homology <XYL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Pathway: xylan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S20907; MUID:92261318; A; Accession: S20907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: A bifunctional xylanase encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Zhang, J.X.; Flint, H.J. Mol. Microbiol. 6, 1013-1023,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Contains: endo-1,4-beta-xylanase (C;Species: Ruminococcus flavefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: Molec
A; Reference number:
A; Accession: S57962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;553-572/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-601 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Start codon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keywords: extracellular protein; glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: Ruminococcus bifunctional endo-1,4-beta-xylanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Function:
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Best Local
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       812
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                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-954 <ZHA>
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S20907; S18043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                       SDDNCDVIYVPGTDGNEEGYELWTTDYDNIPANC---LNKFNEYAVGRETRDVFTSA 168
                                                                                                               NEDEKSIQAEFLFMNNADTNMQFATEKYTAVKMYGYNR--ENAFRYETEDGQVFTDVIAY
                                                                                                                                                      PDWFFRENFSQNGAYVSKDIMNQRLESMIKNTFAALKSQYPNLDVYSYD-VC
                                                                                                                                                                          PDW---ADEAANGAH--QDAW-KSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDGQVFTDVIAYSDDNCDV-----IYVPGTDGNEEGYELWTTD-----YDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEDGKNLDAKDLFLNTDGTINEDTKFTVANGKLIA----YNTEMNEYKKVVVRAYSLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEDEKSIQAEFLEMN-----NADTNMQFATEKVTAVKMYGYNRE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGGYYYADEEDESKEDCEVSSQDDKTSAVQTDVDGN-----LWRLDGGYIYKFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL:Z11127;
ce: strain 17
                                                                              -LFLNNGG-GMRGA-DNSNWVKIYGDDSFVINAFKYARQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   characterization
                                                                                                                                                                                                                                                  8.8%;
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                                                                                                                                                                                                                                  26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID:g46161;
                                                                                                                                                                                                                                              Score 82.5;
Pred. No. 2
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Pred. No. 14;
                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMID: 1584021
                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA77476.1; PID:g581505
                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:CAA90347.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrolase; multifunctional enzyme;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
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                                                                                                                                                                                                                                                                                   C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kra
Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the
A;Reference number: Z14349; MUID:9839469; PMID:98394
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A; Gene: DmRP135
                                                                                                                                                                                                                                                                                                                          A;Gene:
                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF062865; PIDN:AAC83587.1
A;Experimental source: cultivar Columbia
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C;Keywords: DNA binding; nucleotidyltransferase; nucleus; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kontermann, R.; Sitzler, S.; Seifarth, W.; Petersen, G.; Bautz, Mol. Gen. Genet. 219, 373-380, 1989
A;Title: Primary structure and functional aspects of the gene codi A;Reference number: J00354; MUID:90158499; PMID:2482932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jul-2000 C;Accession: J00354; S07025
                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-166 <KRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number:
A;Accession: T51637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 30/3;
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A; Residues: 1-1129 <KON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-directed RNA polymerase (EC 2.7.7.6) I second largest chain - fruit fly
                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                     Superfamily: Arabidopsis 28K leaf-specific myb-related protein;
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                          MYB14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the authors
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                                                                                                                                  6
                                                                                                                                                                                                                                                                                 transcription
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JQ0354
                                                                                                                                                                    WKSLKA------DVENVYYM-VKATYKNDPVWGNDFTCVGVMANDVNEDEKSIQAEFL
                                                        ----TASLQQFSNSITTFDISNDNKDDIMSYE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGAHQDAWKSLKA--DVENVYYMVKATYKNDPV-----W---GNDFTCVGVMANDVNED 59
                                                                                           FMNNADTNMQFATEKYTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDN--CDVIYVPG
                                                                                                                                  WSAIAAKLPGRTDNEIKNVWHTHLKKRLSKNLNNGGDTKDVNGINETTNEDKGSVIVD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESSLSNVVHYLNNGTAKFMFSHVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKSIQAEFLFMNNADTNMQFATEK
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: X17298;
translated th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase:FBgn0003278
                                                                                                                                                                                                                          8.5%;
                                                                                                                                                                                                                                                                                     factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.7%;
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                                                                                                                                                                                                           27;
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                                                                                                                                                                                                                          Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 81.5;
Pred. No. 4:
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
LNKFNEYAVGRETRDVFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:CAA35185.1;
G for residue 202
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                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kranz, H.D.;
                                                                                                                                                                                                           65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
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                                                                                                                                                                                                                                              Length 166
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                                                        DISALIDDSFWSDVISVDN
                                                                                                                                                                                                           Indels
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the R2R3-MYB gene

from

167

126 63 8 38;

Gaps

myb

DNA-binding

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Denekamp,

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Greco,

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A;Gene:
C;Superf
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An:
A:Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein alr2832 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Datc: 14 Dec-2001 #sequence_revision 14 Dec-2001 #text_change 09 Dec-2002 C;Accession: AI2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         명
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C; Superfamily: Arabidopsis 28K leaf-specific myb-related protein; myb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable MYB family transcription factor [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C;Accession: E84717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: AB1807; A; Accession: AI2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: At2g31180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE002093; NID:g4432813; PIDN:AAD20663.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-249 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-362 < KUR>
                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakazaki, N.; Shimpo, S.
NA Res. 8, 205-213, 2001
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                                                                                                                                                                                                                                                             alr2832
                                                                                                                                                                                                                                                                                                                                                                                                       preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
                                              192 SDTKDEYYLASARMISYKRLDIIVEAFNWLGWPLIISGDGPERER-LQAKALDNIKFLGH 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 WKSLKA-----DVENVYYM-VKATYKNDPVWGNDFTCVGVMANDVNEDEKSIQAEFL 68
73
                                                                                           23
                                                                                                                                            . Similarity 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 8.5%; Score 80; DB 2; Length 249; Similarity 22.6%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSAIAAKLPGRTDNEIKNVWHTHLKKRLSKNLNNGGDTKDVNGINETTNEDKGSVIVD-- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDN--CDVIYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNKNEKKIEDWEGLIDRNSKKCSYSNSKLYNDDMEFWF-----DVFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDGNEEGYELWTTDYDNIPANC-----LNKFNEYAVGRETRDVFTS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNKNEKKIEDWEGLIDRNSKKCSYSNSKLYNDDMEFWF-----DVFTS 153
ADTNMQ---FATEK---VTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCDVIYVPG
                                                                                           ADVENVYYMVKA---TYKNDPVWGNDFTCVG---VMANDVNEDEKSIQAEFL----FMNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TASLQQFSNSITTFDISNDNKDDIMSYE-----DISALIDDSFWSDVISVDN 193
                                                                                                                                                                                                                                       hypothetical protein sll1534
                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                          8.5%; Score 79.5; Ilarity 23.6%; Pred. No. 15; Conservative 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.; Sugimoto, M.; Takazawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T.P.; Benito, M.I.; Town, C.D.; Fujil, C.Y. hen, M.; VanAken, S.E.; Umayam, L.; Tallon, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                        В
                                                                                                                                            69;
                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X
                                                                                                                                                                                        Length 362;
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                                                                                                                                            Indels
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                                                                                                                                            41;
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                                                                                                                                                                                                                                                                                                                                GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yasuda, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-binding
                                                                                           72
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Nucleic Acids Res. 29, 2145-2153, 2001.

A;Title: The complete genome sequence of the murine respiratory A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: D90538
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A; Residues: 1-1377 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein MYPU_2120 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                   A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AL445566; PID:g14089625; PIDN:CAC13385.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 MYPU_2120
                                                                                                                                                                      1116 QDAWKS----EDKYYYDQKANQNKTIASQYKLDQKVFKIPKNSKDALKEITFLGTTINLT 1171
1209 NSNGEQIWYRNAQ-NEEAHAV----FKNLLSSDNNSYKGYSLSVDQINAF 1253
                                                                                    1172 INED-KVWRADF-----AD------DKEIDKIKKYYKDLEIQYSFE-------GYT 1208
                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 QTGVFFKRQTPESLQKALLESGEITW--DYENIRNHAVNNFSEPVFFSKVERVITQTC 359
                                                                                                                                                                                                              15 QDAWKSLKADVENVYYMVKAT-----YKND-----PVWGND----FTCVGVMAN-D 55
                                                                                                                            56 VNEDEKSIQAEFLEMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYS 115
                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSDNQRKELFSKAKSIIVAALEDYGL------VPVEANASGTPVIAFGAGGVLDTQING 303
                                        DDNCDVIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVF
                                                                                                                                                                                                                                                                                                                                             SGC3
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                             8.5%; Score 79.5;
24.7%; Pred. No. 83
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                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                               83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V.; Samson, D.; Gallsson, F.; Moszer,
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                                                                                                                                                                                                                                                                                                   Length 1377;
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                                            165
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Job time: 14.7029 secs

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Maximum Match 100%
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Maximum DB seq
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Perfect score:
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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936
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| Ggn2_6/ptcodata/1/pubpaa/US07_PUBCOMB.pep:*
| Ggn2_6/ptcodata/1/pubpaa/PCT_NEW_PUB.pep:*
| Ggn2_6/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*
| Ggn2_6/ptcodata/1/pubpaa/US06_PUBCOMB.pep:*
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15 US-10-278-113-22
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15 US-09-738-626-514-0
15 US-09-815-242-1258-6
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Sequence 5779, Appl
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| 72<br>72<br>73<br>74<br>75<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71<br>71   | 75<br>75<br>72.5<br>72.5<br>72.5<br>72.5<br>72.5  |
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| 0 106, P 0 106, P 0 107, P 0 107, P 0 107, P | Sequence 3284, Ap<br>Sequence 8284, Ap<br>Sequence 8299, A<br>Sequence 5, Appli<br>Sequence 5, Appli<br>Sequence 240, App<br>Sequence 240, App<br>Sequence 240, App<br>Sequence 240, App<br>Sequence 2578, Ap |

## ALIGNMENTS

; SEQ ID NO 7; LENGTH: 171; TYPE: PRT; ORGANISM: FS-HBP 2US-10-085-572-7; APPLICANT: Nuttail, Patricia, Ann
APPLICANT: Nuttail, Guido, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
FILE REFERENCE: 2488-1-03
CURRENT APPLICATION NUMBER: US/10/085,572
CURRENT APPLICATION NUMBER: PCT/GB00/03282
PRIOR APPLICATION NUMBER: PCT/GB00/03282
PRIOR APPLICATION NUMBER: 920674.0
PRIOR FILLING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 8 밁 US-10-085-572-7 Query Match Best Local S Matches 171 Sequence 7, Application US/10085572 Publication No. US20020151499A1 GENERAL INFORMATION: SOFTWARE: FastSEQ for Windows Version 4.0 121 VIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLE 61 61 h 100.0%; Score 936; DB 14; Similarity 100.0%; Pred. No. 1.1e-92; 71; Conservative 0; Mismatches 0; KSIQAEFLEMNNADINMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCD 120 NQPDWADEAANGAHQDAWKSLKADVENYYYMYKATYKNDPVWGNDFTCVGVMANDVNEDE KSIQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCD VIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLE Indels Length 171; 0

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US-10-087-195-7

GENERAL INFORMATION:

Sequence 7, Application US/10087195 Publication No. US20020193306A1

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US-10-085-572-6
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; TYPE: PRT
; ORGANISM: FS-HBP 2
US-10-087-195-7
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Best Local
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                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/085,572
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/GB00/03282
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nuttall, Patricia, Ann
APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
FILE REFERENCE: 2488-1-003
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PRIOR EILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 9920673.2
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 8
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TITLE OF INVENTION: Treatment of Allergic Rhinitis
FILE REFERENCE: 2488-1-004
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CURRENT FILING DATE: 2002-03-01
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                  NQPDWADEAANGAHQDAWKSLKADVENYYYMYKATYKNDPVWGNDFTCVGVMANDVNEDE 60
DKPVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDE 60
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                                                                          Score 630; DB 14;
Pred. No. 7.4e-60;
""" matches 37;
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Query Match

35.48;

Score 331.5;

DB 14;

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; TYPE: PRT
; ORGANISM: MS-HBP
US-10-085-572-8
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US-10-087-195-6
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                                                                 SEQ ID NO 8
LENGTH: 182
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                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/GB00/03282
PRIOR FILING DATE: 2000-08-24
PRIOR FPLICATION NUMBER: 9920674.0
PRIOR FILING DATE: 1999-09-01
NUMBER OF CEC.
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Publication No. US20020151499A1
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CURRENT APPLICATION NUMBER: US/10/085,572
CURRENT FILING DATE: 2002-02-27
                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/087,195
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: PCT/GB00/03287
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nuttall, Patricia, Anne
APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Allergic Rhinitis
FILE REFERENCE: 2488-1-004
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; TYPE: PRT
; ORGANISM: MS-HBP 1
US-10-087-195-8
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                                                                                                                                                                                                                                                                                                                               US-09-728-914-4
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                Sequence 4, Application US/09728914 Patent No. US20010046499A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10087195 Publication No. US20020193306A1 GENERAL INFORMATION:
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Matches 74; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
APPLICANT: DAS, SUBRATA
TITLE OF INVENTION: TICK ANTIGENS AND COMPOSITIONS AND METHODS COMPRISING
TITLE OF INVENTION: THEM
TITLE OF INVENTION: THEM
EILE REFERENCE: YU-107
CURRENT APPLICATION NUMBER: US/09/728,914
CURRENT FILLING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 60/169,048
PRIOR APPLICATION NUMBER: 60/169,048
PRIOR FILLING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/240,716
PRIOR FILLING DATE: 2000-10-16
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PRIOR FILING DATE: 2000-08-24
PRIOR PPLICATION NUMBER: 9920673.2
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 8
SOFTMARE: FastSEQ for Windows Version 4.0
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APPLICANT: Paesen, Guido, Christiaen
TITLE OF INVENTION: Treatment of Allergic Rhinitis
FILE REFERENCE: 2488-1-004
CURRENT APPLICATION NUMBER: US/10/087,195
CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                           APPLICANT: KANTOR, FRED S. APPLICANT: FIKRIG, EROL APPLICANT: DAS, SUBRATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 IQAEFLEMNNADTNMQFATEKVTAVKMYGYNRENAFRYETED -- GQVFTDVIAYSD-DNC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 PDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDEKS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 42.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                             PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Mismatches
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TYPE: PRT
; ORGANISM: Ixodes scapularis
US-09-728-914-4
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US-10-278-173-22
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SEQ ID NO 22
LENGTH: 249
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 4
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Best Local Similarity 24.2%;
Matches 32; Conservative 2
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: MBI-009
CURRENT APPLICATION NUMBER: US/10/278,173
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
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                                                                                                                                                                                                                    ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 TTQIYRVYYPSC 219
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                        147 ----TASLQQFSNSITTFDISNDNKDDIMSYE-----
                                                                                                                                                   18 WKSLKA-----DVENVYYM-VKATYKNDPVWGNDFTCVGVMANDVNEDEKSIQAEFL 68
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                                                                69 FMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDN--CDVIYVPG 126
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                                                                                                           WSAIAAKLPGRTDNEIKNVWHTHLKKRLSKNLNNGGDTKDVNGINETTNEDKGSVIVD--
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Pilgrim, Marsha
Keddie, James
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Ratcliffe, Oliver
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Zhang, James
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                                                                                                                                                                                             Conservative
                                                                                                                                                                                         8.5%; Score 80; DB
22.6%; Pred. No. 1.3;
vative 27; Mismatches
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3; Pred. No. 0.063;
24; Mismatches 69;
                                                                                                                                                                                                                                      DB 15; Length 249;
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US-09-738-626-5144
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SEQ ID NO 5144
LENGTH: 929
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                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                             TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                            ENERAL INFORMATION
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                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                            APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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    APPLICATION NUMBER: US/09/815,242 FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
31; Conserv
                                                                                                             Xu, H. Howard
                                                                                                                                                    Trawick, John D. Carr, Grant J.
                                                                                                                                                                                                   Wall,
                                                                                                                                                                                                                      Zyskind, Judith W.
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TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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                                                                                                                                 amamoto, Robert T.
                                                                                                                                                                                                   Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Fast:
SOFTWARE: Fast:
SEQ ID NO 5484
FUNCTH: 327
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                           PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                      PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                             PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                      NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
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Zyskind, Judith W.
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Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. Howard
for Windows Version
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-PEKILNKMRELA 325

Length 327 Indels

42;

Gaps

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PRIOR APPLICATION NUMBER: US/09/805,354

PRIOR APPLICATION NUMBER: US 09/758,493

PRIOR FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: US 60/221,950

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: DDM
US-10-144-259-17

Sequence 17, Application US/10144259

Publication No. US20030109691A1

GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
APPLICANT: Li, Rui
APPLICANT: Xiong, Jian-Ping
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
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US-09-805-354-17
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LENGTH: 327
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APPLICANT: Arnaout, M. Amin
APPLICANT: L1, Ru1
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Publication No. US20030078375A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xiong, Jian-Ping
TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 007086-536001
CURRENT APPLICATION NUMBER: US/09/805,354
CURRENT FILING DATE: 2002-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 8.4%;
Local Similarity 23.1%;
les 28; Conservative 7
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Pred. No. 1.8;
20; Mismatches
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; ORGANISM: Homo sapiens
US-10-144-259-17
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; ORGANISM: Staphylococcus aureus US-09-815-242-5779
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CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23
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                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 5779
LENGTH: 841
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LENGTH: 241
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Best Local Similarity 23.1%;
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CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: US 09/758,493
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/221,950
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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Zyskind, Judith W.
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Yamamoto, Robert T
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                                                                                                               for Windows Version
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Pred. No. 1.
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Query Match

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Length 841;

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| 137                | 409 DTSKLKDVTDQFDVIYSNDNKTATVDLMKGQTSSNKQYIIQQVAYPDNSSTDNGKIDYTL 468 |
|                    | IDYTL 468  |

Search completed: August 1, 2003, 12:23:45 Job time: 17.9371 secs

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Post-processing: Minimum Match 0%
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US-08-882-704A-5

US-08-882-704A-5

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US-09-148-270A-2

US-09-488-270A-2

US-09-488-270A-2

US-09-488-270A-3

US-09-171-035-368

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Sequence 61, Appl
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CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR PELING DATE: 1997-08-14
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US-08-282-197C-61
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Best Local S
Matches 33
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SEQ ID NO 3207
LENGTH: 337
TYPE: PRT
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                                                                                                                                                                                                                                                                               Sequence 61, Application US/08282197C Patent No. 5871730 GENERAL INFORMATION:
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APPLICANT: Dery, Claude V
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase
TITLE OF INVENTION: Methods of Use
                                                                                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                          ADDRESSEE:
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                             E: Sterne, Kessler,
1100 New York Ave.,
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US-08-448-170-8
US-08-961-803-9
US-08-386-727-4
US-08-600-452A-4
US-09-199-637A-405
US-09-254-733-7
US-09-328-352-6764
US-08-90-751-3
US-08-962-190-2
PCT-US-09-328-352-6764
US-08-962-190-2
PCT-US-08-962-190-2
PCT-US-08-65-10310-2
5164180-4
US-08-100-709-4
US-08-100-709-4
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SEQUENCES RELATING S AND THERAPEUTICS

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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 56, Application PC/TUS9601314 GENERAL INFORMATION:
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                                            FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/31
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                        UMBER OF SEQUENCES:
                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM FC
OPERATING SYSTEM:
                REGISTRATION NUMBER:
                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 29-JUL-1994
                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PDW---ADEAANGAH--QDAW-KSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                           02110-2804
                                                                                                                                                                                                                                                                                         Boston
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                                  John W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cimbala, Michele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDEKSIQAEFLFMNNADTNMQFATEKVTAVKMYGYNR--ENAFRYETEDGQVFTDVIAY 114
                                                                                                                                                                                                                                                                                                   3: Fish & Richardson P.C.
225 Franklin Street
                                                                                                                                                          WordPerfect (Version 5.1)
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          IBM PS/2 Model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202-371-2600
      Freeman 29,066
 NUMBER:
                                                                                                                                                                           MS-DOS (Version
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50z or 55SX
00786/267001
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Query Match
Best Local Similarity
Matches 37; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: JB TELECOMMUNICATION INFORMATION: TELEPHONE: 201-822-7255
                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: U. ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh 6.
OPERATING SYSTEM: Macintosh 6.
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
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LENGTH: 252 amino acids
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                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                            TOPOLOGY:
                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                               NAME: Lunn, Paul G. REGISTRATION NUMBER:
                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 WPNSDPPFSFKNVISLTEDVDEFRNKLQGERISGNLDAPEGGFDAILQTAVCTRDIGWRP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 WGN-----DFTCVGVMANDVNEDEKSIQAEFLFMN-----NADTNMQFAT-----EKV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
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                                                                                                     : 489 amino acids
amino acid
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One Giralda Farms
                                                                                                                                                                                     201-822-7039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                            linear
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              8.2%;
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23.1%;
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                                                                                                                                                                                                                                               32,743
                                                                                                                                                                                                                                                                                            U.S. Patent Application No. 07/980,527 filed November
                                                                                                                                                      1:
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                                                                                                                                                                                                                                 JB0285Q
              Score 76.5;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78.5;
Pred. No. 1
                               DB 5;
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                               Length 489;
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Conservative

30;

Mismatches

Indels

55;

Gaps

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                                                                              ; ANTI-SENSE:
US-08-871-5728-6
               Query Match
Best Local Similarity 19.3
Matches 37; Conservative
                                                                                                                                                                                                TELEFAX: (908) 273-4679 INFORMATION FOR SEQ ID NO:
                                                                                                     TOPOLOGY: un
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-D
SOFTWARE: PATENTIN REL
CURRENT APPLICATION DATA:
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                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MUCCINO, RICHARD 32,538
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                            STRANDEDNESS:
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 4 DWADEAANGAH------QDAWKSLKADV---ENVYYMVKATYKNDPVWGNDF-
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                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCRDGKIGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQDVDVDPETTCYIRVYNVVVRMNG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Schwartz, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mariano, Thomas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cook, Jeffrey
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                                                                                                                               unknown
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N: 435
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                                                                                                                                             unknown
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                                      19.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158
                                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robert
                                                                                                                                                                                                                                                                                                                              US/08/871,572B
                                                                                                                                                                                                   <u>.</u>.
                           29;
                       Score 75.5; DB
Pred. No. 2.5;
29; Mismatches
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                                                 Length 259;
                          Indels 55;
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RESULT 7
5221789-1
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                                                                                                                       STI
                                                                                                                                      Patent No. 5221789

APPLICANT: NOVICK, DANIELA; RUBINSTEIN, MENACHEM

TITLE OF INVENTION: INTERPERON-GAMMA RECEPTOR FRAGMENT AND
                   SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
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  PRODUCTION

PRODUCTION

NUMBER OF SEQUENCES: 1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/578,826

APPLICATE: 07-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/190,204
CURRENT FILING DATE: 1994-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ward, Rebecca H.R.
TITLE OF INVENTION: TREATMENT OF INFAMMATORY BOWEL DISEASE WITH IFN-GAMMA
TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 48
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 07/997,835
PRIOR FILING DATE: 1992-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 11669.90USWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US93/11966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quence 2, Application US/08190204 tent No. 6558661
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LENGTH: 489
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1 Similarity 19.38;
37; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                               VCRDGKIGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCITIFNSSIKG 245
                                                                                                                                                                                                                                                                                     VCITIFNSSIKG
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                                                                                                                                                                                                                                                                                                                                                                  -----SEIQYKILTQKEDDCDEIQCQLAIPVSSLNSQYCVSAEGVLHVWGVTTEKSKE 233
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Pred. No. 6.4;
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US-08-790-912-3
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       Matches
                                           Best Local
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TELEX: 831-494
INFORMATION FOR SEQ ID NO: -3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,939
FILING DATE: 23-SEP-1996
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1964 amino act
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SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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APPLICANT: Plaut, Andrew G.
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: OF STREPTOCCCCUS
                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Leary, Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 76
                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 29-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Philadelphia
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Local Similarity 19.3%;
es 37; Conservation
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                                Similarity
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       Conservative
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SYSTEM: PC-DOS/MS-DOS
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8.0%; Score 74.5; 1
25.2%; Pred. No. 63;
Live 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0,
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                                                                    DB 2;
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   32;
                                                                Length 1964;
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Gaps
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US-08-790-912-2
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 6
FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Weiser APPLICANT: Plaut,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (21. 831-494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME:
                                                                                                                                                                                                                                     1197
                                                                                                                                                                        1246 S-NKQTANKLLLHYNDHSSEKFDLKYQTDFANLP-----EYNLG 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1173 S-NKQTANKLLLHYNDHSSEKFDLKYQTDFANLP-----EYNLG 1210
                                                                                                                                                                                                    113 AYSDDNCDVIYVPGTDGNEEGYEL-WTTDYDNIPANCLNKFNEYAVG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 AYSDDNCDVIYVPGTDGNEEGYEL-WTTDYDNIPANCLNKFNEYAVG 158
                                                                                                                                                                                                                                                                    61 KSIQAEELEMNNADINMQFATEKVTAVKMYGYNRENAFRYETE-----DGQVFTDVI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2, Application US/08790912
5. 5976542
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                                                                                                                                                                                                                                                                                                   l Similarity 25.2 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: PANITCH SCHWARZE JACOBS & NADEL, P.C
1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                             2052 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (215) 567-2991
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25.2%;
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                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                  Score 74.5; D:
Pred. No. 67;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7600-401
                                                                                                                                                                                                                                       -KSTIVKYGNLVKENSLLYQKELLSAVMMKDDQVITDIV 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHODS FOR TREATMENT PNEUMONIAE INFECTION
                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                 Length 2052;
                                                                                                                                                                                                                                                                                                   Indels
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US-09-107-532A-6865
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                                                                 Sequence 6865, Application US/09107532A

Patent No. 6583275

Patent No. 6583275

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5946:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (B) LOCATION 1...420 SEQUENCE DESCRIPTION: SEQ ID NO: 5946:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
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                                         CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 DWDD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 EDEKSIQAEF----LFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 DWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDV-----N 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          --DSTN-----GDGSNSEGY----TDYSSYSENTYDQYQDPNTYYQQTEDTSQYYT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDDNCDVIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNE----YAVGRETRDVFT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDLLSIQNELKKQLNIKTSDTLPNLKNE-----NASMMFFDDSEDG------
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OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
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          GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.9%; Score 74; DB 4; Length 420; 23.3%; Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----MLDVATNYTPAFETIKQDQLQGE-----GQMINDIYYQILGK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
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                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-107-532A-4711
Sequence 4711, Application US/09107532A
PATENT NO. 6583275
GENERAL.INFORMATION:
APPLICANT: Lynn A Doucette-Stamm an
TITLE OF INVENTION: NUCLEIC ACID ANG
BUTTEROCCCCUS FAI
NUMBER OF SEQUENCES: 7310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTE
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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 IYVPG--TDGNEEGYELWTTDYDNIPANCL-NKFNEYAVGRETRDVFTS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 FLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYS-----DDNCDV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VSYPGEVTHGKKRTYYKIT----EIGRNLLEEKKQEWLT---TKDVVTS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FQVMEYADTMMRLFYRSFNKNDSYGYEISKTIRERTNDSYVIKETTLYSVFARLEKNQLI 60
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FILING DATE: 14 MBy 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: PC
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                                                                                                                                                                                                       STATE: Massachusetts
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                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                      CITY: Waltham
                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterocóccus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                           ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02354
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Pred. No. 1.3;
8; Mismatches
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NO: 6865:
                                                                                                                                                                                                                                                                                                                                                                                                        and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
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SOFTWARE: ASCII

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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3716
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                                           Query Match
                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3716
      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3716, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                        APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
                                                                                                                          TYPE: PRT
                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
/ Match 7.8%; Score 73; DB Local Similarity 23.7%; Pred. No. 53; es 36; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: ATINIELLO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: (B) LOCATION 1...489 SEQUENCE DESCRIPTION: SEQ ID NO: 4711:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 DFEFIYPIVEATYSDLGRPSIDPV---
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                                                                                                                                            1335
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32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SDDNCDVIYVPGT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (781)893-827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 489 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-Jun-1998 APPLICATION DATA:
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Pred. No. 11;
                                         DB 4; Length 1335;
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46;
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  Indels
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52;
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Gaps
9;
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08882704A Patent No. 5879906
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                        APPLICANT: Wilson, KE APPLICANT: Leader, M: TITLE OF INVENTION: ON SEQUENCES:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CORRESPONDENCE ADDRESS:

STREET: ADDRESSEE:

6300 Columbia Center,

701 Fifth Avenue

SEED and BERRY LLP

Seattle Washington

COUNTRY:

USA

98104-7092

APPLICANT:

Jefferson, Richard A. Wilson, Katherine J. Leader, Michael

GLUCURONIDE REPRESSORS AND USES THEREOF

CURRENT APPLICATION DATA:

| Ŋ   | 19 K                    | KSIKAD-VENVYYMVKATYKNDPVWGNDFTCVGVWANDVNEDEKSIQAEFLFMNN 72  |    |
|---|-------------------------|---|----|
| ъ   | 329 K                   | KNMKAPRIEEDYTSYFPKYGYRNGVGRPEGIVVHDTANDNSTIDGEIAFMKR 380  | ő  |
| Σ¥  | 73 A                    | ADTINGFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCDVIYVPGT 127   | ?7 |
| ъ   | 381 -                   | AGP 41  | F  |
| λγ .                                      | 128 D                   | DGNEEGYELWTTDYDNIPANCLNKFNEYA 156   |    |
| ъ   | 412 Y                   | YGNQRFINVEIVHTHDYDSF-ARSMNNYADYA 442  |    |
| SECULT 14                                 |                         |   |    |
| 1268463-2<br>1268463-2                    | л<br>Э                  | 2002  |    |
| APPLI                                     | CANT:                   | APPLICANT: JEFFERSON, RICHARD A.<br>TITLE OF INVENTION: PLAANT PROMOTER a-GLUCURONIDASE GENE                      |    |
| CONSTRUCT                                 | 3                       |   |    |
| CURRE                                     | NT AP                   | CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/07/447.976  |    |
| PRIOF                                     | FILING DATE:            | FILING DATE: 08-DEC-1989 PRIOR APPLICATION DATA:  |    |
| APF<br>FII                                | APPLICATION FILING DATE | APPLICATION NUMBER: 119,102 FILING DATE: 10-NOV-1987 ADDITCATION NUMBER: 264 586                                  |    |
| FILING<br>SEQ ID NO:2:                    | FILING DATE:            | ATE: 31-OCT-1988  |    |
| LEN<br>1268463-2                          | LENGTH: 600             | 600   |    |
| Query Match<br>Best Local :<br>Matches 4: | tch<br>al Sin<br>41;    | 7.7%; Score 72.5; DB 6; Length 600; illarity 23.4%; Pred. No. 19; Conservative 26; Mismatches 55; Indels 53; Gaps | 10 |
| Ϋ́  | 1<br>- <u>X</u>         | QPDWADEAANGAHQDAWKSLKADVENVYYMV 32  |    |
| ř   | 368 NI                  | 8 NKPKELYSEEAVNGETQQAHLQAIKELIARDKNHPSVVMWSIANEPDTRPQVHGNISPLA 427  | 7  |
| γ   | 33 K                    | KATYKNDPVWGNDFTCVGVMANDVNEDEKSIQAEFLFMNNADTNMQFATEKVTAVKMYGY 92   |    |
| ŏ   | 428 E                   | ATRKLDPT RPITCVNVMFCDAHTDTISDLFDVLCLNRYYGW 469  | 9  |
| Ϋ́  | 93 NI                   | NRENAFRYETEDGQVFTDVIAYSDDNCDVIYVPGTDGNEEGY-ELWTTDY 141  |    |
| ŏ   | 170 Y                   | 470 YVQSG-DLETAEKVLEKELLAWQEKLHQPIIITEYGVDTLAGLHSMYTDMWSEEY 523   |    |
|   |                         |   |    |
| IS-08-882-704A-5                          | 704A-                   |   |    |

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APPLICATION NUMBER: US/08/882,704A
FILING DATE: 25-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5879906tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6011
TELEFAX: (206) 622-
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000_DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000_DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOPDWADEAANGAHQDAWKS.....FNEYAVGRETRDVFTSACLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
                                                                                                                                                                                                                                                                                                             Length
190
190
172
172
190
190
                                                                                                                                                                                                                                                                                                             ВB
   ij
                                AAB74289
AAB73261
AAW37447
AAY18079
AAB74288
AAB74260
AAW37446
AAW37446
                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (without alignments)
511.236 Million cell updates/sec
                      Histacalin protein
Histacalin protein
Tick vasoactive am
Histamine binding
Histacalin protein
Histacalin protein
Tick vasoactive am
Histamine binding
                                                                                                                                                                                                                                                                                       Description
Histacalin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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## ALIGNMENTS

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RESULT 1
AAB74289
  Use of histacalin proteins for treating or preventing non-infective conjunctivitis, or for manufacturing a medicament for treating or preventing conjunctivitis, e.g. seasonal or perennial allergic conjunctivitis
                                                                                                                                                                                                                          Histacalin; FS-HBP1; conjunctivitis.
                                                                                                                                                                                                                                                Histacalin protein FS-HBP2
                                                                        Nuttall PA, Paesen GC;
                                                                                                                   01-SEP-1999;
                                                                                                                                       24-AUG-2000; 2000WO-GB03282.
                                                                                                                                                              08-MAR-2001.
                                                                                                                                                                                   WO200115719-A2
                                                                                                                                                                                                       Unidentified.
                                                                                                                                                                                                                                                                     20-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                           AAB74289;
                                                                                                                                                                                                                                                                                                                AAB74289 standard; protein; 171 AA.
                                                                                              (EVOL-) EVOLUTEC LTD
                                                    2001-257675/26
                                                                                                                   99GB-0020674.
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protein

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RESULT 2
AAB73261
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Best Local S
Matches 171
 Query Match
Best Local
                                                    The present invention relates to a method for treating or prevent allergic rhinitis. The method involves employing a blood-feeding ectoparasite-derived (e.g. tick-derived) histacalin protein. The sequence is one such histacalin protein. The histacalin protein, useful for treating or preventing allergic rhinitis, both seasons perennial allergic conjunctivitis.
                                                                                                                                                      Use of histacalin proteins for treating or preventing allergic rhinitis, or for manufacturing a medicament for treating or preventing allergic rhinitis, e.g. seasonal or perennial allergic rhinitis -
                                   Sequence
                                                                                                                                     Disclosure;
                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                    08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                             Nuttall PA,
                                                                                                                                                                                                                                                   (EVOL-)
                                                                                                                                                                                                                                                                        01-SEP-1999;
                                                                                                                                                                                                                                                                                              24-AUG-2000;
                                                                                                                                                                                                                                                                                                                                         W0200116164-A2
                                                                                                                                                                                                                                                                                                                                                                                  opthalmological;
                                                                                                                                                                                                                                                                                                                                                                                               FS-HBP2; histacalin
                                                                                                                                                                                                                                                                                                                                                                                                                      Histacalin
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1s
1n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB73261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB73261 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r treating or preventing conjunctivitis. The present sequence the histacalin protein FS-HBP1. The invention is particularly useful the treatment of allergic or seasonal conjunctivitis.
                                                                                                                                                                                                      2001-218521/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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Similarity
                                                                                                                                                                                                                                                  EVOLUTEC LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSIQAEFLFMNNADINWQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOPDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSIQAEFLFMNNADTNMQFATĖKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 5-6;
                                   171
                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                     Pages 4-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                              2000WO-GB03287.
                                                                                                                                                                                                                           Paesen
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                                   B
                                                                                                                                                                                                                                                                        99GB-0020673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                  lin protein; antiinflammatory;
allergic rhinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 171
                                                                                                                                                                                                                                                                                                                                                                                                                    FS-HBP2
                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relates to the
                                                                                                                                    19pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                   English.
 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 936; DB 22;
Pred. No. 1.6e-89;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
 936;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use of a histacalin
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                                                                                                                                                                                                                                                                                                                                                                                              antiallergic;
         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                  seasonal and
                                                                                                            preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                        present
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ARESULT 3
AAW37447
ID AAW3
AC 
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                                                                                                                               This protein comprises tick Rhipicephalus appendiculatus (Ra) novel female-specific histamine binding protein 2 (FS-HBP2). Its amino acid sequence was deduced from a cDNA clone (see AAV00228) obtained from a salivary gland cDNA library. FS-HSP1 (see AAW37446) and male-specific HSP1 (see AAW37448) and a related protein, D.RET6 (see AAW37449) from Dermacenter reticularis, were also identified. These novel vasoactive amine binding proteins (VABPs) can be expressed in host cells using e.g. a baculovirus expression system. They can be used: (i) to assay histamine (or other VA such as serotonin) in be used: (i) to assay histamine (or other VA such as serotonin) in
anti-inflammatory agents, e.g scorpion bites or dermatitis,
                                                       body fluids or cell culture supernatants, e.g. to monitor the effect of allergens; (ii) for binding VA, e.g. to remove histamine from blood, food, cell cultures etc.; (iii) as an antihistamine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New vasoactive amine binding proteins and related nucleic acid, vectors - transformed cells and transgenic animals, used for assaying or removing histamine and as antihistamine or anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV00228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-018506/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-1997;
18-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuttall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Female-specific vasoactive amine binding protein 1; FS-HCP1; histamine; serotonin; assay; antihistamine; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW37447 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OXFO-) OXFORD VACS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9744451-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhipicephalus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW37447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insect bite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vasoactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLE
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                                                                                                                                                                                                                                                                                                                                                                                                          Fig 2; 44pp;
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96GB-0010484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Sig_peptide
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tick.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding
                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scorpion
                           e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                              for treating insect,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bite;
        carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                              snake or
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RESULT 4
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ស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្រីស្ត្
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Matches 171
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                   This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and sectonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rininitis; atopic dermatitis; food allergy; abnormal blood pressure; psychological disorder; vaccine respiratory disease; coronary heart disease; cellular growth regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1999
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                                                                                                                                                                                                                    Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histamine
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                                                                                                                                                                                                                                                                                                 Histamine and serotonin binding compounds useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histamine binding protein; serotonin binding compound;
(e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OXFO-) OXFORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-1998;
26-NOV-1997;
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97GB-0025046.
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Pred. No. 1.8e-89;
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Query Match Best Local S Matches 113

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                                           The present invention relates to the use of a histacalin protein for treating or preventing conjunctivitis. The present sequence is the histacalin protein FS-HBPL The invention is particularly in the treatment of allergic or seasonal conjunctivitis.
                                                                                                                                                                                                                             Use of histacalin proteins for treating or preventing conjunctivitis, or for manufacturing a medicament for preventing conjunctivitis, e.g. seasonal or perennial conjunctivitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EVOL-) EVOLUTEC LTD.
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                                                                                                                                                                          4; Page 5-6;
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AAB73260
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                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                         Matches
                                                                                                                                                                                                                                         The present invention relates to a method for treating or preventing allergic rhinitis. The method involves employing a blood-feeding ectoparasite-derived (e.g. tick-derived) histacalin protein. The present sequence is one such histacalin protein. The histacalin protein, is useful for treating or preventing allergic rhinitis, both seasonal and
                                                                                                                                                                                                                                                                                                                                           Use of histacalin proteins for treating or preventing allergic rhinitis, or for manufacturing a medicament for treating or preventing allergic rhinitis, e.g. seasonal or perennial allergic rhinitis.
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                       Disclosure; Pages 4-6; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200116164-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FS-HBP1; histacalin protein; antiinflammatory; antiallergic; opthalmological; allergic rhinitis.
                                                                                                                                                                                                                                 perennial allergic
                                                                                                                                                                                                                                                                                                                                                                                                                              Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2000; 2000WO-GB03287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Histacalin protein FS-HBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB73260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB73260 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EVOL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                    2001-218521/22.
 121
             121 VIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                   61
                                                                                                                                                       113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVOLUTEC
                                                                                                               NQPDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDE
VIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVYTSDCL
                                                 KNVEAWFMEMNNADTVYQHTFEKATPDKMYGYNKENATTYQTEDGQVLTDVLAFSDDNCY
                                                              KSIQAEFLFMNNADINMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCD
                                                                                                  DKPVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVYTSDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSIQAEFLEMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKPVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDE
                                                                                                                                                                                                          172
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Paesen GC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                         A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99GB-0020673
                                                                                                                                                                                                                                 conjunctivitis.
                                                                                                                                                                  67.3%;
                                                                                                                                                     20;
                                                                                                                                                   Score 630; DB 22;
Pred. No. 1.3e-57;
0; Mismatches 37;
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                                                                                                                                                                             Length 172;
                                                                                                                                                     Indels
                       170
 170
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RESULT 7
AAW37446
                                                           CC female-specific histamine binding protein (FS-HBP1). Its amino CC female-specific histamine binding protein (FS-HBP1). Its amino CC acid sequence was deduced from a cDNA clone (see AAV00227) obtained CC from a salivary gland cDNA library. FS-HSP2 and male-specific CC HSP1 (see AAW37447-48) and a related protein, D.RET6 (see AAW37449) CC from Dermacenter reticularis, were also identified. These novel CC management of the second of the second in D.RET6 (see AAW37449) CC from Dermacenter reticularis, were also identified. These novel CC constitute amine binding proteins (VABPS) can be expressed in CC be used: (i) to assay histamine (or other VA such as serotonin) in CC body fluids or cell culture supernatants, e.g. to monitor the CC from blood, food, cell culture supernatants, e.g. to monitor the CC from blood, food, cell cultures etc.; (iii) as an antihistamine or CC corpion bites or dermatitis, or as a carrier for slow release of instamine-related compounds; (iv) in vaccines to protect against CC metazoan parasites, esgencially in animals; (v) as reagents for CC immune response etc. VABPs provide a more sensitive assay for histamine than low-affinity antibodies currently used. They may called the process of the stamine of the content of the con
Sequence
                                                 also be more effective and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assaying or removing histamine and as antihistamine anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       histamine; serotonin; assay; antihistamine; anti-in: insect bite; snake bite; scorpion bite; dermatitis; transgenic animal; tick.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 1; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vasoactive amine binding proteins and related nucleic acid, vectors - transformed cells and transgenic animals, used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Female-specific vasoactive amine binding protein 1; FS-HCP1;
histamine; serotonin; assay; antihistamine; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tick vasoactive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OXFO-) OXFORD VACS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhipicephalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-018506/02.
DB; AAV00227.
190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paesen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amine binding protein 1 FS-HBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Sig_peptide
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                                                 safer than
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                                                 conventional antihistamines
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NQPDWADEAANGAHQDAWKSLKADVENYYYMYKATYKNDPVWGNDFTCVGVMANDVNEDE

Query Match Best Local S Matches 113

al Similarity 66.5 113; Conservative

67.38;

20;

Score 630; DB Pred. No. 1.5e 20; Mismatches

DB 19; L.5e-57; les 37;

Length 190; Indels

0

Gaps

60 0;

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ANYIBOTA RESULT 8
ANYIBOTA ANY
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                                                                                                                      Query Match
Best Local !
                                                                                           Matches
                                                                                                                                                                                                                                                                                    This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease), Histamine may also be used as components of vaccines directed against blood-sucking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhipicephalus
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                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histamine and serotonin binding of allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuttall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OXFO-)
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26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Histamine binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amine binding protein; serotonin binding compound; inflammation; rick acid secretion; allergy; type I hypersensitivity reaction; ma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; map; urticaria; allergy abnormal blood pressure; psychological disorder; vaccine allergy; abnormal blood pressure; psychological disorder; vaccine tractory disease; coronary heart disease; cellular growth regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-357841/30.
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                                                                                        al Similarity
113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Fig 1; 84pp;
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NOPDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVWANDVNEDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVYTSDCL
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                                                                                                                                                                                                        190
                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VACS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blood-sucking ectoparasite;
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97GB-0025046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein FS-HBP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ရှ
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                                                                                                                67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                        20;
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                                                                                     Score 630; DB 20;
Pred. No. 1.5e-57;
O; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compounds
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                                                                                                                                              Length
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                                                                                     Gaps
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RESULT 10
AAB73262
ID AAB73
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AAB74290
ID AAB7
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Best Local
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                    Use of histacalin proteins for treating or preventing conjunctivitis, or for manufacturing a medicament for preventing conjunctivitis, e.g. seasonal or perennial
                                                                                                                                                                                                                                                                                                                              The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Histacalin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Histacalin
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 5-6; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        conjunctivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EVOL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2001.
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                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                               the treatment of
                                                                                                                                                                                                                                                                                               the histacalin
                                                                                                                                                                                                                                                                              present invention relates to the use of a histacalin protein treating or preventing conjunctivitis. The present sequence the histacalin protein FS-HBPl. The invention is particularly the treatment of allergic or seasonal conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-257675/26.
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                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVOLUTEC LTD.
                                                                             PDWADEAANGAHQDAWKSLKADVENYYYMYKATYKNDPVWGNDFTCVGVMANDVNEDEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACL 170
DVIEVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSC
                                DVIYVPGTDGNEEG-YELWTTD--YDNIPANCLNKFNEYAVGRE--TRDVFT-SAC
                                                               LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIYALGPDGSGAGYELWATDYTDVPASCLEKFNEYAAGLPVRDVYTSDCL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKPVWADEAANGEHQDAWKHLQKLVEENYDLIKATYKNDPVWGNDFTCVGTAAQNLNEDE
                                                                                                                         PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSIQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein MS-HBP1
                                                                                                                                                                                                                                                  182 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paesen
                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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                                                                                                                                                                                                     35.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conjunctivitis
                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                     Score 331.5; DB Pred. No. 2e-26;
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                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                     g non-infective
r treating or
l allergic
                                                                                                                                                                                      11;
                                                                                                                                                                                      Gaps
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                              169
   175
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AAB73262

standard;

protein; 182

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
       Male-specific vasoactive amine binding protein 1; MS-HCP1; histamine; serotonin; assay; antihistamine; anti-inflammatory; insect bite; snake bite; scorpion bite; dermatitis; vaccine; transgenic animal; tick.
                                                                      Tick vasoactive
                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for treating or preventing allergic rhinitis. The method involves employing a blood-feeding ectoparasite-derived (e.g. tick-derived) histacalin protein. The presensequence is one such histacalin protein. The histacalin protein, is useful for treating or preventing allergic rhinitis, both seasonal and perennial allergic conjunctivitis.
                                                                                                08-JUN-1998
                                                                                                                         AAW37448;
                                                                                                                                                  AAW37448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of histacalin proteins for treating or preventing allergic rhinitis, or for manufacturing a medicament for treating or preventing allergic rhinitis, e.g. seasonal or perennial allergic rhinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MS-HBP1; histacalin protein; antiinflammatory; antiallergic; opthalmological; allergic rhinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuttall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EVOL-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Histacalin protein MS-HBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB73262;
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                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVOLUTEC LTD
                                                                                                                                                standard;
                                                                                                                                                                                                          DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSC
                                                                                                                                                                                                                                  DVIYVPGTDGNEEG-YELWTTD--YDNIPANCLNKFNEYAVGRE--TRDVFT-SAC
                                                                                                                                                                                                                                                             LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNC
                                                                                                                                                                                                                                                                                                                                   PDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDEKS 62
                                                                                                                                                                                                                                                                            IQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETED--GQVFTDVIAYSD-DNC 119
                                                                                                                                                                                                                                                                                                           PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK
                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paesen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99GB-0020673
                                                                     amine binding
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                                                                                                                                                Protein;
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                                                                                                                                                                                                                                                                                                                                                                          35.4%;
                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                200
                                                                                                                                                                                                                                                                                                                                                                          Score 331.5; DB Pred. No. 2e-26;
                                                                      protein 1 MS-HBP1
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                      BB
                                                                                                                                                                                                                                                                                                                                                              62;
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                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                      182;
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                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                               from a salivary gland cDNA library. Female-Specific HSP1 and
HSP2 (see AAW37446-47) and a related protein, D.RET6 (see AAW37449)
from Dermacenter reticularis, were also identified. These novel
vasoactive amine binding proteins (VABPs) can be expressed in
be used: (i) to assay histamine (or other VA such as serotonin) in
body fluids or cell culture supernatants, e.g. to monitor the
from blood, food, cell cultures etc.; (iii) as an antihistamine or
anti-inflammatory agents, e.g. for treating insect, snake or
scorpion bites or dermatitis, or as a carrier for slow release of
histamine-related compounds; (iv) in vaccines to protect against
metazoan parasites, especially in animals; (v) as reagents for
studying inflammation, involvement of VA in ulcer formation or the
immune response etc. VABPs provide a more sensitive assay for
histamine than low-affinity antibodies currently used. They may
                                                                                                                                                                                Matches
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This protein comprises tick Rhipicephalus appendiculatus (Ra) numale-specific histamine binding protein 1 (MS-HBP1). Its amino acid sequence was deduced from a cDNA clone (see AAV00227) obta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New vasoactive amine binding proteins and related no vectors - transformed cells and transgenic animals, assaying or removing histamine and as antihistamine
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-018506/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 3; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-1997;
18-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-мат-1997;
                                                                                                                                                                                                                                                                       be more effective and
 138
                             120
                                                           78
                                                                                       63
                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXFORD VACS LTD
                                                                                                                                                                                              Similarity
DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSC
                 DVIYVPGTDGNEEG-YELWTTD--YDNIPANCLNKFNEYAVGRE--TRDVFT-SAC
                                                                                                      TWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK
                                                                                                                                      PDWADEAANGAHQDAWKSLKADVENYYYMYKATYKNDPVWGNDFTCVGVMANDVNEDEKS
                                                         LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNC
                                                                          200 AA;
                                                                                                                                                                             35.4%; ilarity 42.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paesen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             appendiculatus
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96GB-0010484
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79..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Asn is N-glycosylated"
                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                      safer than conventional antihistamines
                                                                                                                                                                             Score 331.5; DB 19
Pred. No. 2.3e-26;
9; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                related nucleic c animals, used :
                                                                                                                                                                                                            DB 19;
                                                                                                                                                                              Indels
                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c acid,
                                                                                                                                                                                                            200
                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel
                                                                                                                                                                             Gaps
193
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RESULT 12 AAY18080

77

62

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Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gabtric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermititis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            ectoparasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Histamine and serotonin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-1998;
26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9927104-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhipicephalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Histamine binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histamine binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY18080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY18080 standard; Protein; 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OXFO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999-357841/30
  138
                                              120
                                                                                            78
                                                                                                                                        63
                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX76966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OXFORD
                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 3; 84pp;
                                                                                                                       IQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETED--GQVFTDVIAYSD-DNC 119
                                                                                                                                                                                                               PDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDEKS
DVIYVPGTDGNEEG-YELWTTD--YDNIPANCLNKFNEYAVGRE--TRDVFT-SAC
                                                                                            LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSDYKNC
                                                                                                                                                                                       PTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIG--KKK
                                                                                                                                                                                                                                                                                                                                                                                200
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paesen GC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     appendiculatus.
                                                                                                                                                                                                                                                                                                                                                                                Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VACS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0013917
97GB-0025046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-GB03530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein MS-HBP1
                                                                                                                                                                                                                                                                                                         35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serotonin binding compound;
                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                         Score 331.5;
Pred. No. 2.3
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compounds useful for the treatment
                                                                                                                                                                                                                                                                                 1.3e-26;
nes 62;
                                                                                                                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation;
                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                   Gaps
                                                169
  193
                                                                                                                                                                                         77
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RESULT 13 AAY18085

5 В Ş 밁 Š

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S

D-DNCDVIYVPGTDGNEEGYELWT-TDY-DNIPANCLNKFNEYAVGRETRDVFTSACL 170

8

DGQTCDLLYIP---YKENGYELWVRSDYLQNTPTCCQFIFDLVALGRTTYNISTPDCV

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В
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                                                                                                                                           Query Match
Best Local :
                                                                                                                            Matches
                                                                                                                                                                                                                 This sequence is an example of a histamine or serotonin binding compound (A), of the invention. cDNA encoding this sequence was isolated from a mixed Boophilus microplus/Ixodes hexagonus cDNA expression library. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rininitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking ectoparasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 7; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histamine and serotonin binding compounds useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9927104-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boophilus microplus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue repair; blood-sucking ectoparasite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histamine binding protein; serotonin binding compound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histamine binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-1999
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-1998;
26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ixodes hexagonus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY18085 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OXFO-) OXFORD VACS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-357841/30
DB; AAX76970.
                               56
                                                              27
                                                                                                                            63;
                                                                                                                                            Similarity
                               VNEDEKSIQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYS 115
                                                              NEPLKNTTWHSKELKN--YQDAWKSINQNVSTTYYFLRSTYNNDSVWGKNFTCLSVTVTS
                                                                                           NQP----DW-ADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMAND
                                                                                                                                                                                          203 AA;
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paesen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0013917.
97GB-0025046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                         30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ih/Bm-HBP1
                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203
                                                                                                                                           Score 288;
Pred. No. 8.
                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ξ
                                                                                                                                           DB 20;
.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy
                                                                                                                                                        Length
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation;
                                                                                                                                                             203;
                                                                                                                            14;
                                                                                                                            Gaps
                                                              84
   143
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198

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AAY18086
ID AAY1
XX
AC AAY1
XX
AC AAY1
XX
DE Hist
XX
Hist
XX
WW Hist
KW gast
KW gast
KW Gru
KW Hist
KW Gru
KW Hist
KW Gru
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                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from a mixed Boophilus microplus/Ixodes hexagonus CDNA expression library. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking ectoparasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Histamine and serotonin binding compounds useful for the treatment of allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Fig 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boophilus microplus. Ixodes hexagonus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-1998;
26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9927104-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY18086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY18086 standard; Protein; 203 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OXFO-) OXFORD
                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                        57
                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                    Similarity
-DNCDVIYVPGTDGNEEGYELWT-TDY-DNIPANCLNKFNEYAVGRETRDVFTSACL 170
                                                          YESTFTVEYNTTYKNQSQQWVSM-SENVTAVQEGGYSVKNIIQWTTENNTKFNDTVVFTD
                                                                                                                  NEDEKSIQAEFLFMNNADINMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSD 116
                                                                                                                                                                                                               NQP----DWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDETCVGVMANDV
                                                                                                                                                                                NEPLEKTTWHNQTL-GRYQDAWKSINQSVGTTYYFLRSTYNNDSVWGKNFTCLSVTVTSK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (A)
                                                                                                                                                                                                                                                                                                                                                                                                                           203
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paesen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of.
                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VACS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98GB-0013917.
97GB-0025046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-GB03530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an example of a histamine or serotonin binding the invention. cDNA encoding this sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein Ih/Bm-HBP2.
                                                                                                                                                                                                                                                                                                                                 30.4%;
                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                 Score 285; DB 20;
Pred. No. 1.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ectoparasite;
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                203;
                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated
                                                                                                                                                                                                                                          56
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Query Match Best Local S Matches 66

Similarity

30.1%;

Score 282; DB 19; Pred. No. 3.6e-21; 9; Mismatches 69;

Length 209; Indels

12;

Gaps

8

Conservative

29;

Sequence

209

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and safer than

conventional antihistamines.

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RESULT 15
AAW37449
                                                                      vABPs can be expressed in host cells using e.g. a baculovirus of the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                         This protein comprises tick Dermacenter reticularis (Dr) novel vasoactive amine binding protein (VABP) D.RET6. Its amino acid sequence was deduced from a cDnA clone (see AAV00230) obtained from a Dr salivary gland cDNA library. 3 Novel VASPs, designated FS-HBP1, FS-HBP2 and MS-HBP1 (see AAW37446-48), of the tick Rhipicephalus appendiculatus have also been identified. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New vasoactive amine binding proteins and related nucleic vectors - transformed cells and transgenic animals, used f assaying or removing histamine and as antihistamine or anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vasoactive amine binding protein; D.RET6; histamine; serotonin; assay; antihistamine; anti-inflammatory; insect bite; snake bite; scorpion bite; dermatitis; vaccine; transgenic animal; tick.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-018506/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW37449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 4; 44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuttall PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009841; AAL63753.1;
Hypothetical protein; Complete proteome.
SEQUENCE 476 AA; 53745 MW; EAB3000C5244C280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
PubMed-11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprote1; Thermoproteales; Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
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Q8ZWE9;
Q1+MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PAE1819.
PAE1819.
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                                                                                                                                                                         114 VKAVFQYGYKNIRNAIEYQVG------------GGLNITDTLIFTDGELCDVF 154
                                                                                                                                                                                                         149 -----GELIKAKDLVVEKLLYKDKVKGITSVAPALERIVVTTKNATSDRKPDPNATET 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 IFSGDHDMEVPYL----GTQAWIRSLNYSLIDDWRPWMIGDQIAGYTRTY 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 IFTDGELCDVFYVPNADQGCELWVKKSHYKHVPDYCTFVFNVFCAKDRKTY 194
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                                                                   248 YTPNYLNISGCTLGFTGMLYGSIPVIVTAWHCSF 281
                                                                                                                                        202 IKKKI----KEIDSDLEVEVAYAEEARPTLSRGSVFNPLVGGINI--TLIYR-----
                                                                                                                                                                                                                                          65 ENDTGSWGSQFKC--LQVQEIERKEEDYTVTS-----VFTFRNASSPIK-YYNVTET 113
                                                                                                                                                                                                                                                                               99 VLVLDIDYTAVLAT ------GNSSPYWRNYTVIKAWELTWN--NQTARVYQVRLRWSY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 ELLGKYQDAWKSIDQGVSVT-----YVLAKTTYENDTGSWGSQFKCLQVQEIE 84
                                                                                                                                                                                                                                                                                                                                            n 7.6%; Score 85; DB 17; Length 476;
Similarity 24.3%; Pred. No. 31;
52; Conservative 29; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                   VVLLLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTY 64
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Best Local
  Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K., Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J., Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL844505; CAD50567.1; ...
SEQUENCE 6761 AA; 797061 MW; 7000C644C420A246 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998
01-JAN-1998
01-MAR-2003
                                                                                                              SEQUENCE FROM N.A.
Cherevach I., Davis P.,
                                                                                                                                                                                   Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
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"InlB : an invasion protein of Listeria
type of surface association.",
Mol. Microbiol. 25:285-294(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes 
Bacteria; Firmicutes;
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InterPro; IPR002502; Amidase_2.
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'; SM00644; Ami_2; 1.
'NCE 917 AA; 102352 M
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                                                                                                   "Full-Length cDNA from Arabidopsis thaliana. Submitted (MAR-2002) to the EMBL/GenBank/DDB EMBL; AC011560; AAG51371.1; -. EMBL; AC013428; AAF76347.1; -. EMBL; AV088751; AAM67067.1; -. HSSP; P10619; 117Y.
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnst
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F18K10 genomic
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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O9SQX6:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat putative glucose acyltransferase.
F13M14.27 OR F18K10.3.
                         InterPro; IPR001563; Serine_carbpept.
Pfam; PF00450; serine_carbpept; 1.
PRINTS; PR00724; CRBOXYPTASEC.
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Feldmann K.A., Flavell R.B., White O.,
"Full-length messenger RNA sequences g
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591790; CAC46962.1;
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_dep_Rec; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
putative outer membrane receptor protein.
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                                            TDG-----ELCDVFYVPNADQGCELWVKKSHYKHVPD-YCT
                                                                                             TYLGLTLDDFKDTPFRRYNASQKDVIDAAHNIYQFSH-----SYEITPDINLTTTVYR
                                                                                                                                            TFRNAS-----SPIKYYN-----VTETVKAVFQYGYKNIRNAIEYQVGGGLNITDTLIF
                                                                                                                                                                                                 DGFKDIDRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSRFVEYKIDEKKGTVQQVWEYGKERGYDFYSPITSVIEYQKDRDTMFGFGGSINLFDVG 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DTGSWGSQFKCLQVQEIERKEEDYTVT------SVFTFRN------ASSPIK
                                                                                                                                                                                                                                          DAWKSIDQGVSVTYVLAKTTYENDTG----SWGSQ--FKCLQ-VQEIERKEEDYTVTSVF
TDTTRAWYKLNDV -- RNDSDTG -- - WVSLSNILADPDTYST
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22; AAK31641.1; -.
                                                                                                                                                                                              101872 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                 24;
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                         Score 86.5;
Pred. No. 55;
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                                                                                                                                                                                                                                                                                                 Mismatches
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356
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RESULT
Q8XMD0
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Best Local :
                     Query Match
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01-MAR-2002
01-MAR-2002
                                                     Schirmer A., Jendrossek D.;

**Molecular characterization of the extracellular poly(3-hydroxyoctanoic acid) [P(3HO)] depolymerase gene of Pseuc fluorescens GKI3 and of its gene product.*;

J. Bacteriol. 176:7065-7073(1994).

EMBL; U10470; AAA64539.1;

Hypothetical protein; Signal.

SIGNAL 1

26

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmic Clostridium. NCBI_TaxID=1502;
                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2002 (TrEMBLrel. 20, Last annotation
Hypothetical 63.2 kDa protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. EMBL; AP003188; BABB0465.1; ... Hypothetical protein; Complete SEQUENCE 399 AA; 46802 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein CPE0759. CPE0759.
                                             SEQUENCE
                                                                                                                                             MEDLINE-95050280; PubMed-7961472;
                                                                                                                                                            STRAIN-DSM 7139;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 Q51717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-13 / Type A;
PubMed-11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                          Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=294;
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           Similarity
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(TrEMBLrel.
(TrEMBLrel.
                                             584 AA;
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irmicutes; Clostridia;
 Conservative
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46802 MW;
                                             63249 MW;
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          7.68;
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                                                                                                                                                                                                                 Gammaproteobacteria; Pseudomonadales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
 15;
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Last sequence Last anno
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Pred. No. 20;
Pred. No. 33;
5; Mismatches
                     Score 86;
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61019F007582B815 CRC64;
                                             3AA16FAE898D2CBF CRC64;
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51;
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Best Local S
Matches 59
                                                                                                                                "Salp25D, an Ixodes scapulum immunodominant antigens in engorged J. Infect. Dis. 184:0-0(2001).
EMBL; AF209913; AAK97816.1; -. SEQUENCE 221 AA; 25359 MW; 7B99
                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TremBLrel. 19, 01-DEC-2001 (TremBLrel. 19, 01-OCT-2002 (TremBLrel. 22, Histamine binding protein.
                                                                                                                                                                                                                                                                Ixodes scapularis (Black-legged tick) (Deer tick)
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arac
Parasitiformes; Ixodida; Ixodidae; Ixodes.
                                                                                                                                                                                                                                                                                                    HBP.
                                                                                                                                                                                                                                                                                                                                                            Q95WZ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Rhode Island; TISSUE-Salivary gland; Valenzuela J.G., Francischetti I.M., Pham V.M., Mather T.N., Ribeiro J.M.C.;
                                                                                                                                                                                                       Fikrig
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF483718; AAM93640.1; -.
                                                                                                                                                                                                                                                     NCBI_TaxID=6945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                              l Similarity
49; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59;
                                                                                                                                                                                                                  Banerjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
WRTYD-VTDFSGNPVQCENFRVMEKR----TPTNYSFQYRYKSKN-SWETIDETLILKDI
                                             TYGSTGTTTRPGTRGARMIVTTAPPEEDP
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                      KTTYENDTGSWGSQFKCLQVQEIERKEEDYTVTSV-FTFRNASSPIKYYNVTET--VKAV
                                                                     TFVSAALATQAET----TSAKAGENPLWAHEELLGKY--QDAWKSIDQGVSVTYVLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFSTPLCYVVRSLQDDEGYESCEFWLSEDWLKKNVTIPQVVTILEKEDSDEIEKSEEREE
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                                                                                                                                                                         an Ixodes scapularis antioxidant, is one of 14 inant antigens in engorged tick salivary glands
                                                                                                                                                                                                                                                                                                                                                                                                                                                           199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 AA;
                                                                                              Conservative 43;
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                                                                                           Score 97.5; D
Pred. No. 0.89
13; Mismatches
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                                             -SKYKEQNATRVVE--MNATQWVK
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                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 311;
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Q8IDR7;
01-MAR-2003
SEQUENCE FROM N.A.
STRAIN=MB4-8242;
MSTRAIN=MB4-82731; PubMed=11534764;
Kang J.W., Jeong Y.J., Kwon A.R., Yun H.J., Kim D.H., Choi "Cloning, sequence analysis, and characterization of the a encoding an arylsulfate sulfotransferase from Citrobacter
                                                                                                                                                          Enterobacteriaceae;
NCBI_TaxID=546;
                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                                                                      Arylsulfate
ASTA.
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Hypothetical protein.
SEQUENCE 972 AA; 119242 MW; 70471A60C0327C32 CRC64;
                                                                                                                                                                                                                               Citrobacter freundii.
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Eukaryota; Alveolata;
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43; Conserv
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01-CCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-20
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-Rhode Island; TISSUE-Salivary
Valenzuela J.G., Francischetti I.M.,
Mather T.N., Ribeiro J.M.C.;
"Exploring the Stalome of the Tick Ve
scapularis.";
                                                                                                                                         Submitted (FEB-2002)
EMBL; AF483717; AAM93
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EMBL; AF483742; AAM93
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AAM93664.1; -.
                                                                                                                                         2002) to the EMBL/GenBank/DDBJ AAM93639.1; -.
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46; Conserv
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QBMVC2;

QBMVC2;

Q1-OCT-2002 (TrEMBLrel. 22, Created)

Q1-OCT-2002 (TrEMBLrel. 22, Last sequence update)

Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)

PULTATIVE secreted histamine binding protein.

Ixodes scapularis (Black-legged tick) (Deer tick).

Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachni
Parasitiformes; Ixodida; Ixodidae; Ixodes.

(NCBI_TaxID-6945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

TISSUE-Salivary gland;

MEDLINE-21317941; PubMed-11425229;

MEDLINE-21317941; PubMed-11425229;

Mans B.J., Venter J.D., Vrey P.J., Louv

"Identification of putative proteins in

tick salivary glands.";

Electrophoresis 22:1739-1746(2001).

EMBL; AF452891; AAN76331.1;

SEQUENCE 176 AA; 19375 MW; 44B75591
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Eukaryota; Metazoa;
Parasitiformes; Ixo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
30; Conserv
                                                                                                                                                                                                                                                                    LQMKTSPFPGKCELWAPEGKAKNVESSCSGKFKELC
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Hetazoa; Arthropoda; Chelicerata;
Hetazoa; Argasidae; Ornithodo
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1; Mismatches
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                                                     Arachnida; Acari;
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Result
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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Perfect score:
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                                  1125
126
117.5
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1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_invertebb:
6: sp_mammal:*
7: sp_mhae:*
10: sp_phage:*
11: sp_rodent:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebra
 100.0
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Match
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Gapop 10.0 ,
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1 MKMQVVLLLTFVSAALATQA.....DRKTYDIFNEECVYNGEPWL 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_archea:*
sp_bacteria:*
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sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                         sp_organelle:*
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sp_unclassified:*
sp_rvirus:*
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sp_archeap:*
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sp_rodent:*
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Q8XMD0
Q51717
Q33983
Q8IC77
Q9SQX6
Q8ZWE9
                                                                                     Q8WSK7
Q8MV98
Q8MVC3
Q819T9
Q819T9
Q8MVC2
Q95WZ5
Q81DR7
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                             OBwsk7 dermacentor
OBmv98 ixodes scap
OBmv98 ixodes scap
OBJ949 ornithodoro
OBmvc2 ixodes scap
OSJ972 ixodes scap
OSJ972 ixodes scap
OSJ972 citrobacter
OSZ9747 rhizobium m
OSJ717 pseudomonas
OSJ983 listeria mo
OBJC77 plasmodium
                                                                                                                                                                                        Description
Q9sqx6 arabidopsis
Q8zwe9 pyrobaculum
Q9en29 amsacta moo
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| Q8tq07 methanosarc | 17 Q8TQ07 | 310  | 7.1 | 79.5 | 5        |
|--------------------|-----------|------|-----|------|----------|
|                    | 16 Q8R6U4 | 267  | 7.1 | 79.5 | 4        |
| Q91hk6 papaya ring | 12 Q91нк6 | 3343 | 7.1 | 80   | ω        |
| 087818 roseobacter |           | 262  | 7.1 | 80   | ັນ       |
| Q97tq5 clostridium | 16 Q97TQ5 | 434  | 7.2 | 81   | Ξ        |
| Q8zn12 salmonella  |           | 1092 | 7.2 | 81.5 | ö        |
| Q9s003 borrelia bu | 2 Q9S003  | 370  | 7.2 | 81.5 | 9        |
| Q9kk99 rickettsia  | 2 Q9KK99  | 1604 | 7.3 | 82   | 8        |
| Q8iavl plasmodium  | 5 Q8IAV1  | 1210 | 7.3 | 82   | 7        |
| Q59290 clostridium | 2 Q59290  | 930  | 7.3 | 82   | 5        |
|                    | 5 Q9W034  | 876  | 7.3 | 82   | ŭ        |
|                    | 2 Q9JN39  | 713  | 7.3 | 82   | <u>~</u> |
|                    | 2 Q937B8  | 637  | 7.3 | 82   | ũ        |
|                    | 5 Q95Y41  | 564  | 7.3 | 82   | ວ        |
| a                  | O         | 561  | 7.3 | 82   | ĩ        |
|                    |           | 390  | 7.3 | 82   | õ        |
|                    |           | .360 | 7.3 | 82   | 9        |
|                    | 16 Q97DZ8 | 163  | 7.3 | 82   | 8        |
| 031976 bacillus su |           | 2285 | 7.4 | 83   | 27       |
| 064046 bacteriopha | 0         | 2285 | 7.4 | 83   | 6        |
| Q8fn80 corynebacte |           | 644  | 7.4 | 83   | Ğ        |
| Q8ic57 plasmodium  | 5 Q81C57  | 2879 | 7.4 | 83.5 | 4        |
| Q8jrx7 phthorimaea |           | 1133 | 7.4 | 83.5 | ũ        |
| 002158 caenorhabdi | 0         | 482  | 7.4 | 83.5 | 2        |
| xenop              |           | 386  | 7.5 | 84   | 2        |
|                    | 5 Q95WY8  | 218  | 7.5 | 84   | õ        |
| Q8wsj2 bombyx mori | Ö         | 1801 | 7.5 | 84.5 | 9        |
| Q8y496 listeria mo | 16 Q8Y496 | 917  | 7.5 | 84.5 | 8        |
| O50272 listeria mo | 2 050272  | 917  | 7.5 | 84.5 | 7        |

## ALIGNMENTS

| Qу<br>Db   | Qy<br>Db  | Qy  | Query M<br>Best Lo<br>Matches   |   |  |  | RT by   |   | RP SEQ             |                   | OC Pa   |  |  |             |             |                                    | ID 081                           | RESULT : |
|--|---|---|---|---|--|--|---|---|--------------------|-------------------|---|--|--|-------------|-------------|------------------------------------|----------------------------------|----------|
| 121 GYKNIRNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNADQGCELWVKKSHYKHVPDYCT 180<br> | 61 KTTYENDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYYNVTETVKAVFQY 120<br> | 1 MKMQVVLLLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQDAWKSIDQGVSVTYVLA 60<br> | Query Match 100.0%; Score 1125; DB 5; Length 209;<br>Best Local Similarity 100.0%; Pred. No. 5.6e-92;<br>Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | Pfan; PF02218; His. Dinding; 1. Pfan; PF02218; Linding; 1. SEQUENCE 209 AA; 23889 MW; E5EB8BE710859591 CRC64; | EMBL; AF217101; AAL56644.1; Interpro: TPR002970: His hinding | Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. | "A High allinity seroconin- and histamine-binding iipocaiin secreted<br>by blood-feeding ticks."; | Sangamnadech S., Paesen G.C., Nuttall P.A.; | SEQUENCE FROM N.A. | NCBI_TaxID=57047; | Parasitiformes; Ixodida; Ixodidae; Dermacentor. | Eukarvota: Metazoa: Arthropoda: Chelicerata: Arachnida: Acari: | Serotonin and histamine binding protein. | (TrEMBLrel. | (TrEMBLrel. | -MAR-2002 (TremBLrel: 20; Created) | Q8WSK7 PRELIMINARY; PRT; 209 AA. |          |

Search completed: August 4, 2003, 17:15:10 Job time : 25 secs

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RESULT 14
DNAK_RACOPA
ID DNAK_RACOPA
AC 09ZDX9
AC 09ZDX9
DT 30-MAY
DX RICKET
OC Bacter
OC Ricket
OC Bacter
OC Ricket
OC Bacter
OC Ricket
OC Ricket
OC NCBLIT
RN 11
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DR MATURE
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                                                                 Query Match
Best Local S
Matches 33
                                                                                                                                                                                              HAMAP; ME_00332; -; 1.
InterPro; IPRO01023; Hsp70.
Pfam; PF00012; Hsp70; 1.
PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; Hsp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99039499; PubMed-9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                             EMBL; AJ235270; CAA14651.1;
PIR; D71729; D71729.
HSSP; P04475; 1DG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsia prowazekii.
Rickettsia; Proteobacteria; Alphaproteobacteria;
Bacteria; Proteobacteria; Alphaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chaperone protein dnaK (Heat shock protein 70)
                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome sequence mitochondria,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-Madrid E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ZDX9;
30-MAY-2000
                                                                                                                                                   Complete proteome. MOD_RES 197
                                                                                                                                                                              Chaperone; ATP-binding; Heat shock; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein) (HSP70).
DNAK OR RP185.
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                                                                                                                                                                                                                                                                                                            HAMAP; MF_00332;
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   10
                            72 GSQFKCLQVQE-----IERKEEDYTVTSVFTFRNA----SSPIKYYNVTETVKAVFQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                 Similarity
GTTNSCVAVMEGKEPKVIDNAEGERTTPSIIAFANSERLVGQPAKRQAVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LWVKKSHYKHV 175
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                                                                                                                                  627 AA;
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KGELWALTAGWRQKHAKNKVLRFEPASTSGGVCWNPLDEIRLGTEYEVGDVQNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                   197
                                                                                                                                  68383 MW;
                                                                               7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334
                                                                 15;
                                                              Score 81.5; D
Pred. No. 12;
15; Mismatches
                                                                                                                                PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
; A638A0A5A5C8ACC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                DB
                                                                42;
                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsiales;
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                                                                                              Length 627;
                                                                Indels
                                                                27;
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                                                              Gaps
 59
                                 121
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Query Match
Best Local
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HS9C_DICDI
P54651;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00775; HEATSHOCK90.
SMART; SM00387; HATPASE_C; 1.
PROSITE; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L43591; AAA69917.1; -.
HSSP; P07900; 1YER.
DictyDb; DD00051; hspD.
InterPro; IPR003594; ATDbind_ATPase.
InterPro; IPR001404; Hsp90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02518; HATPase_c; 1. Pfam; PF00183; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1995) to the EMBL/Ge-1- FUNCTION: MOLECULAR CHAPERONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat shock cognate 90 kDa protein.
HSPD OR HSC90.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
15-DEC-1998 (Rel. 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boves H., Dittrich W., Mintert U., Lottspeich F., Gerisch G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-AX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                          142
368
                              191
                                                                                                                         248
                                                                                                                                                                                       188
                                                                                                                                                                                                                                                 128 FYSAYLVADTVIVHSKNNDDEQYVWESSAGGEFTIALDHTEPLGRGTKIVLHMKEDQLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 YKNIRNAIEYQVGG--GLNITDTLIFTDGELCDVFYVPNADQGCELWVKKSHYKHVP 176
                                                                                                                                                      92
                                                                                                                                                                                                                     43
                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                    QDAWK------SIDQGVSVTYVLAKTTYENDTGSWGSQFKC-LQVQEIERKEEDYT
                                                                                                                                                                                                                                                                                 FVSAALATQAETTSAKAG--ENPLWA-----
RETLQQNKILTVIRKNLVKKCIELFNE
                                                                                                                                                      V---TSVFTFRNASSPIKYYNVTETVKAVFQYGYKNIRNAIE-----YQVGGGLNITD 141
                                                          ILFVPKKAPFDLFESKKKANNIKLYVKRVFIMDNCADIIPEYLNFVRGIVDSEDLPLNIS
                                                                                         TLIFTDGELCDVFYVPNADQGCELWVKKSHYKH-----VPDYCTFVFNVFCAKD-----
                                                                                                                       VKVQEKEWDVLNKTKPLWTRNPSDVTKEEYNSFYKSISNDWEEPLAVKHFSVEGQLEFKA
                                                                                                                                                                                     LDETKIKNLVKKHSEFIQYPISLLTIKEKEVDEETTAKEGEEESTDAKIEEIEEEKEKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --NPRNTI-YAVKRLIGRNFTDPMVRKDQGLVP-YNIVKADNG-DAWVEADNHKYSP 111
                                                                                                                                                                                                                                                                                                                                                                         ATP-binding; Heat shock 700 AA; 79881 MW; BFB
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                             7.2%;
19.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                32;
                             -RKTYDIFNE 199
                                                                                                                                                                                                                                                                                                                           Score 81;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases PERONE. HAS ATPASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                          BFB5ECF238089CD3 CRC64;
                                                                                                                                                                                                                                                                                                                Mismatches
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394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      700
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15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                 ----HEELLGK---
                                                                                                                                                                                                                                                                                                              105;
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                                                                                                                                                                                                                                                                                                                                          Length 700,
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                              78;
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                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                 187
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RESULT
RIR2_CA
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Best Local
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                                                                                                                                                               ACT_SITE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAEEL
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation updat Ribonucleoside-diphosphate reductase small
                                                                                                                                                                                      METAL
                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                              EMBL; Z35637; CAA84688.1; PIR; T18876; T18876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>+ + +</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Ribonucleotide reductase). RNR-2 OR C03C10.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIR2_CAEEL P42170;
                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                          Oxidoreductase;
                                                                                                                                                                                                                                                                                                         WormPep; C03C10.3; CE00874.
                                                                                                                                                                                                                                                                                                                   HSSP; P11157; 1XSM.
                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995
                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                   am;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: BINDS 2 IRON IONS (BY SIMILARITY).
PATHWAY: DNA replication pathway; first steps
SUBUNIT: Heterodiner of a large and a small chain.
SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thioredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                    Pro: IPR000358; Ribonucl_redctse.
Pr00268; ribonuc_red_sm; 1.
TE; PS00368; RIBORED_SMALL; 1.
reductase; DNA replication; Iron.
                        95
                                             58
                                                                   35
                                                                                          9
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLRNII-----GDLELDQTL--TSREMINTQLREVLDEATDKW 148
                                            VLAKTTYENDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPI-----KYYNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIRNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNADQGCELW
                        TVEEVDLGKDMNDW---
                                                                    LEIVDQTKAASAEETNNESEVNELDADEPMLQDLDNRFVIFPLKHHDIWNFYKKAVASFW
                                                                                          LTFVSAALATQAETTSAKAGENPLWAHEELLG------KYQDAWKSIDQGVSVTY
                                                                                                                7.3%;
nilarity 21.8%;
Conservative 2
                                                                                                                                                                                      130
161
164
224
258
261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peloderinae;
                                                                                                                                                                ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                      161
164
224
258
                                                                                                                                                                44289 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nematoda; Chromadorea;
Inae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                 20;
                                                                                                                Score 82; DB
Pred. No. 5.9;
0; Mismatches
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BY SI
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IRÓN 1 (BY SIMILARITY).
IRÓN 1 (BY SIMILARITY).
IRÓN 2 (BY SIMILARITY).
IRÓN 2 (BY SIMILARITY).
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BY SIMILARITY.
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                        EKMNGDEQYFISRILAFFAASDGIVNENLCERFSNE
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small chain
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                                                                                                                          DB
5.9;
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                                                                                                                 56;
                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (E)
                                                                                                                 Indels
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                                                                                                                                       381;
                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL
                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                           outstation
                                                                                                                Gaps
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                                                                                                                                   RESULT 13
TRG5_ECOLI
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Best Local
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01-FEB-1994
28-FEB-2003
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or send a
                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence and organization origin of promiscuous plasmid RP4."; DNA Seq. 1:303-327(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92190548; PubMed-1665997;
Ziegelin G., Pansegrau W., Strack
Kruft V., Lanka E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conjugal transfer protein
                                                                                                                                                                                                     Plasmid;
                                                                                                                                                                                                                EMBL; X54458; CAA38327.1; -. EMBL; U67194; AAC64474.1; -. InterPro; IPR003688; TRAG. Pfam; PF02534; TRAG; 1.
                                                                                                                                                                                                                                                                                              modified and this statement
                                                                                                                                                                                                                                                                                                                                                                    <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid IncP-beta R751.
                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200184;
                                                                                                                                   SEQUENCE
                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
- SUBUNIT: May :
similarity).
                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE VIRD4/TRAG
                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 nitted (AUG-1996) to the EMBL/GenBank/DDBJ databases. FUNCTION: Required for conjugative transfert of plasmid R751. Binds tightly and specifically to the relaxase trai. Can also to DNA, without sequence specificity. May form a pore-like structure that could serve as a channel for DNA transfer (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _ECOLI
                                                                                                                                                                                                                                                                                                                                                                              (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 VQVSEARFFYGFQ
150
                    38
                                           90
                                                                u
                                                                                        46;
                                                                                                                                                                                                                                                                        s requires a license agreement (So an email to license@isb-sib.ch).
                                                                                                  Similarity
                                                         VVLLLTFVSAALATQAETTSAKAGE----NPLWAHEE---
                                                                                                                                                                                                     Conjugation;
PTATGVYVGGWQDKDGNFFYLRHSGPEHVLTYAPTRSGKGVGLVVPTLLSWGASSVITDL
                     --LLGKYQDAWKSID---
                                           LVSTVGLLGVAVAKVVTSNSSKANEYLHGSARWAEKKDIQAAGLLPRERNVLEIVTGKAA
                                                                                                                              106
637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coli.
                                                                                       Conservative
                                                                                                                                   AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                           22
43
84
105
637
69883
                                                                                                                                                                                                                                                                                                                                                                                                               form multimers of at least 18 subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28, Created)
28, Last sequence up
41, Last annotation
                                                                                                                                 n; DNA-binding; Transmembrane; Inner me
22 CYTOPLASMIC (POTENTIAL).
43 POTENTIAL.
84 PERIPLASMIC (POTENTIAL).
105 POTENTIAL.
105 POTENTIAL.
637 CYTOPLASMIC (POTENTIAL).
63883 MW; 7B45A9A9020902FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                           institutions as long
                                                                                                  18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                         Integral membrane
                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strack
                                                                                                                                                                                                                                                                                                is not removed.
                                                                                                  Pred.
                                                                                                            Score 82;
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                     QGVSVTYVLAKTTYENDTG-----
                                                                                       Mismatches
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on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Balzer D.,
                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                            DΒ
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                                                                                                                                                                                                                                                                                               Usage
                                                                                       ; 68
                                                                                                            Length 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      flanking the transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriales;
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RESULT 10
HTPG_RAICPR
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Best Local 9
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30-MAY-2000 (Rel. 3
28-FEB-2003 (Rel. 4
Chaperone protein h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mature 396:133-140(1998).
Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsia prowazekii.
Rickettsia; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                                                                                                                                                                                                                       Chaperone;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00505; -; 1.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR001404; Hsp90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Madrid E;
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                               SMART; SM00387; HATPASE_C; 1. PROSITE; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; H71645; H71645.
HSSP; P02829; 1A4H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ235273; CAA15264.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTPG_RICPR Q9ZCB9;
                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTPG OR RP840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
    127
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                                                                                                                                                                                                                                                                                                                                                                                            PF00183;
                                                    11
                                                                                                   Similarity
39; Conser
YSSFMVADKVTVTSRKAGESKVHTWESDGLGEYIVADSEQEFTRGTEIVLYIKKSETTFL
                                               FVSAALATQAETTSAKAGENPLWAHE-ELLGKY--QDAWKSIDQGVSVTYVLAK--TTYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMKALWTKSKDEVSEDEYKEFYKHIAHAWDDPLEVIAMKAEGTFEYQ-----
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                                                                                                                                                                                            329
545
621 AA;
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                                                                                              7.5%;
llarity 18.9%;
Conservative 4
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41, Last annotation update)
htpG (Heat shock protein htpG)
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                                                                                                                                                                                               MW;
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                                                                                              core 84.5; DE red. No. 6.4; Mismatches
                                                                                                                                                                                            9F97B97801524007 CRC64;
                                                                                                                                                                                                                                         SIMILARITY).
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                                                                                                                                                                                                                                                                  SIMILARITY)
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                                                                                              Gaps
    186
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Matches 38
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026788;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadch R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Yiwani N., Caruso A., Bush D., Safer H., Parwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                      SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND 7; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                          InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
                                                                                                                                                                                                                                                                                                          EMBL; AE000848; AAB85197.1; -. PIR; C69192; C69192.
                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                           PRINTS; PR00721; STOMATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
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                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanobacterium thermoautotrophicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001
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                                     VLLVLAFKSLKILRPYEKGVV
    ENDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIK-YYNVTETVKAVFQYGYK 123
                                                                   VVLLLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTY
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                                                                                                                                                                 318 AA;
                                                                                                  Conservative
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(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                 35425 MW;
                                                                                                                   7.3%;
                                                                                                  23;
                                                                                                 Score 82.5; Di
Pred. No. 4.3;
23; Mismatches
                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                 4A72C0AC8E99278D CRC64;
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                                    -ERLGKYQ---RTVESGLVVIIPFIEAIK 55
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FlyBase; Fr
G0:000;
G0: G0:000
G0: G0:000
G0: G0:000
G0: G0:000
G0: G0:000
G0: G0:000
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EMBL;
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GO:0005737; C:cytoplasm; IDA.
GO:0007349; P:cellularization; IMP.
GO:0009795; P:embryonic morphogenesis; IMP.
GO:0008583; P:mystery cell fate differentiation (sensu Dr...
GO:0007097; P:nuclear migration; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L; L04959; AAF01345.1; -.
L; L04958; AAF01346.1; -.
L; L04960; AAF01348.1; -.
L; AE003779; AAF57198.1; -.
L; AE003779; AAR57198.1; -.
L; AE003779; AAR58652.1; -.
L; AF145677; AAD38652.1; -.
CPS; C19.007; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId-P55824-3; Sequence-VSP_005269;
TISSUE SPECIFICITY: EYE DISKS AND OVARIES.
DEVELOPMENTAL STAGE: Expressed both maternally and
SIMILARITY: Belongs to peptidase family C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conjugation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0006512;
                                                            168
                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00443; UCH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P55824-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :0006512; P:ubiquitin cycle; ro; IPR001394; UCH-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
KRVCVKKLPPVLAIQLKRFEYDYERVCAIKEN------
                                                                                                                                                                                                                                                                 LK---ALGQPQLMNATLGGSFSDQKICQECPHRYSKEEPFSVFSV-DIRNHSS-----L
                                                                                                                                                                                                                                                                                                                          VSVTYVLAKTTYENDT - - GSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYYNV
                                                                                                                                                                                                                                                                                                                                                                                                         VVILKHVQAIFAHLGHSALQYYVPRGLWTHFKLLGEPVNLREQQDAVEFFMSLLESLDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLLLTFVSAALATQAETTSAKAGENPLWAHEELLG-----KYQDA------WKSIDQG
                                                            KKSHYKHVP-----
                                                                                                                                                                                                 TETVKAVFQYGYKNIRNAIEYQVGGGLNITDTLIFTDGEL----CDVFYVPNADQGCELWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pation pathway: Hydrola

htal protein: Vision: J

1677 1677 BY

1978 1978 BY

1986 1986 BY

2705 2778 KCI
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2725
2778
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2725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86; DB
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP_005269.
IATAATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ
IATAATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ
IATAATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ
IATAATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ
IATAATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ
IATAATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ
IATAATLEISTATTMVEKNLIISQENPQAKSSLQ
IATAATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ
IATAATLEPAGMSELTM
I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n; Alternative splicing.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
KCRRVIIKKLVESKDEEDATTATTAATTEVTTSPATAIATA
ATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ -> VTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNV (in isoform 3).
                                          -b¥---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          > D (IN REF. 1).
> S (IN REF. 1; AAF01345).
FFB90438BA53A02B CRC64;
                                                            -CTFVFNVFCAKDRKTYDIFNEECVYNGEPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thiol protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                YVKGELLEGADAYHCDKCDKKV-VTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zygotically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
1942
                                                                                                                                1896
                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                 1865
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                                                                                                                              Query Match
Best Local
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.
                                                                                                                                                                                                                                                                                                                                                                PIR; A87112; A87112.
HSSP; P07900; 1BYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998
15-JUL-1998
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              PRINTS; PR00775; HEATSHOCK90.
SMART; SM00387; HATPase_c; 1.
PROSITE; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                                                    HSSP; P07900; 1BYQ.
Leproma; M11623; -.
HAMAP; MF_00505; -; 1.
InterPro; IPR003594; ATPbin
InterPro; IPR001404; Hsp90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Massive gene decay in the leprosy Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein G).
HTPG OR ML1623 OR MLCB250.19C
                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                    Chaperone;
DOMAIN
                                                                                                                                                                                                                                                                                         Pfam; PF02518; HATPase_c; 1. Pfam; PF00183; HSP90; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Molecular chaperone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chaperone protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTPG_MYCLE
                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
 194
                             66
                                                                                    11
                                                                                                                 1 Similarity
49; Conserv
                                                                         FVSAALATQAETTSAKAGENPL--WAHEELLGKYQDAWKSID----QGVSVTYVLAKTTYE
DELHDYTSEWKIRELVKKYSDFIAWPIRMEVERRAPATSDGEGADGEEQVTIETQTI--N
                                                        YSSFMVANKVELLTRKAGETAATRWSSD----GEATYTIESVDEAPQGTSVTLHLKPEDFE
                           NDTGSWGSQFKCLQV----
                                                                                                                                                                                                  ATP-binding; Heat shock; Complete proteome.

1 359
A; SUBSTRATE-BINDING (BY SIMILARITY).
360
575
B (BY SIMILARITY).
                                                                                                                                                                         576
656 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 36, Creace,
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Geat shock protein htpG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 36, Created)
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                        575 B
656 C
73866 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacteriaceae; Mycobacterium
                                                                                                                              7.6%;
21.3%;
                                                                                                                                                                                                                                                                                                                                   ATPbind_ATPase.
                                                                                                                 38;
                                                                                                              Score 85; DB
Pred. No. 6.2;
88; Mismatches
                                                                                                                                                                                       ဂ ဗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                         A526690CA66E03FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacillus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Has ATPase activity
                           -QEIERK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  656
                                                                                                                                            DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales;
                                                                                                                 79;
                                                                                                                                           Length 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (High temperature
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By
                             EEDYTVTSVFTFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamlin N.,
                                                                                                                 64;
                                                                                                               Gaps
                           100
 251
                                                        193
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AF_DROME

PAF_DROME

AC P55824; Q9Y976; Q9Y0Z7;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT (Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease FAF) (Deubiquitinting enzyme FAF) (Fat facets protein).

DE FAF) (Deubiquitinting enzyme FAF) (Fat facets protein).

GN FAF OR BCDNA:LDZ582 OR CG1945.

OS Drosophila melanogaster (Fruit fly).

CC Neoptera; Endopterygota; Arthropoda; Haxapoda; Insecta; Pterygota;

""hvdroidea; Drosophilidae; Drosophila.

""hvdroidea; Drosophilidae; Drosophila.

""" TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δõ
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Best Local :
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STRAIN-Berkeley;
STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Ev
Amanatides P.G., Scherer S.E., Li P.W.,
Amanatides P.G., Scherer S.E., Richards S., A
                                                                                                                                           MEDLINE=93202020; PubMed=1295747; Fischer-Vize J.A., Rubin G.M., Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; TP0984; -.

HAMAP; MF_00505; -; 1.

InterPro; IPR003594; ATPbind_ATPase.

InterPro; IPR001404; Hsp90.
                                                                                                                  development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chaperone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00387; HATPase_c; PROSITE; PS00298; HSP90; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001265; AAC PIR; F71258; F71258
                                                                           SEQUENCE FROM N.A.
                                                                                                                            "The fat facets gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00775; HEATSHOCK90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires
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TP0984; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVLLLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQD-----AWKSIDQGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYKPGVKLFVKRVFITDDEKELLPVYLRFVRGVIDSED 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D--QGCELWVKK-----SHYKHVPDYCTFVFNVFCAKD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTETVKAVFQYGYKNIRNAIEYQVGGGLNITDTLIFTDG--ELCDVFYVP-----NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTDTQKKVDQVNDAGALWKRPKS-----ELKEEDYHRFYQTLT----RDSTPPLLYVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTYVLAKTTYENDTGSWGSQFKCLQVQEIERKEEDY-----TVTSVFTFRNASSPIKYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVLHLSQENSEFATR------WRLEEVIKKYSDHIAFPIYLHYLQKEYDKDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Heat shock;
1 348 A; SUBS
349 565 B (BY S
566 639 C.
639 AA; 72937 MW; 3E8FD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                   116:985-1000(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC65938.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%;
22.9%;
                                                                                                                               ż
                                                                                                                             required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87;
                                                                                                                                           Lehmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3E8FDBAC2282C31D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBSTRATE-BINDING (BY
                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                            Drosophila
      Evans C.A., Gocayne J.D.,
., Hoskins R.A., Galle R.F.,
Ashburner M., Henderson S.N.,
                                                                                                                                           R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AEGTQEYVTLFYVPAKAPFDLFHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 639
                                                                                                                             eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY
                                                                                                                             and
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                                                                                                                             embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                    protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Debart M.M., Glasser K.,
RA Gebahos B., Dolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., McLeod M.P., McPherson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Show M., Shue B., Wang A.H., Wang X.,
RA Walliams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wall S.M., Ra Markilla M., Kaled M., Shue B., Zhang STRAIN-Berkeley;
MEDLINE-20196012; PubMed-10731138;
Hand L., Brokstein P., Evans-Holm M., ÷ <del>-</del> "Annotation of the Drosophila melanogaster systematic review."; Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E. Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., "A Drosophila complementary DNA resource."; Science 287:2222-2224(2000). Rubin G.M., Hong L., Brokstein Stapleton M., Harvey D.A.; SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM Stapleton M., Yamada Lewis S.E.; MEDLINE=22426069; PubMed=12537572; STRAIN=Berkeley; REVISIONS, FUNCTION: REQUIRED FOR EXE AND EMBRYO DEVELOPMENT, AND PLAYS A ROLE IN COMPOUND EYE ASSEMBLY AND GENESIS RESPECTIVELY. IN THE LARVAL EXE DISKS, CELLS OUTSIDE THE ASSEMBLING FACETS REQUIRE THIS PROTEIN FOR SHORT-RANGE CELL INTERACTIONS THAT PREVENT THE MYSTERY CELLS FROM BECOMING PHOTORECEPTORS. IT IS ALSO REQUIRED FOR NUCLEAR MIGRATION AND CELLULARIZATION IN EARLY EMBRYOGENESIS AND COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR FUNCTION.
CATALYTIC ACTIVITY: ubiquitin + a thiol.
ALTERNATIVE PRODUCTS: Biol. AND ALTERNATIVE SPLICING. 3: RESEARCH0083.1-RESEARCH0083.22(2002) Ubiquitin C-terminal thiolester euchromatic Frise genome: a + в.р., H.O., K.A.,

Event=Alternative splicing; Comment=Experimental

confirmation

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Named isoforms=3; may

IsoId=P55824-1;

Sequence=Displayed

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STRAIN-ATCC 35210 / B31;

STRAIN-ATCC 35210 / B31;

MEDLINE-99065943; PubMed-9403685;

MEDLINE-99065943; PubMed-9403685;

MEDLINE-99065943; PubMed-9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Fraser C.M., Casjens S., Huang W.M., Dodson R., Hickey E.K., Gwinr Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Teland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B
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HTPG_BO
P42555;
                                                                                                                                                                                                                                                                                                                                                                                                                               *Conservation of gene arrangement and an unusual organization of genes in the linear chromosomes of the Lyme disease spirochaetes Borrella burgdorferi, B. garinii and B. afzelii. *;
**Microbiology 140:2931-2940(1994).**
-I- FUNCTION: Molecular chaperone. Has ATPase activity (Bv similarity)
  EMBL;
EMBL;
EMBL;
HSSP;
TIGR;
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HTPG OR BB0560
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01-OCT-1996 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                               between
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; AE001157; AAC66919.1; F
; L32145; AAC41403.1; -,
; P07900; 1YER.
; BB0560; -.
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                                                                                                   U51878; AAA97469.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390:580-586(1997)
                                                                                                                                               non-profit institutions as long d and this statement is not removed. s requires a license agreement (See an email to license@isb-sib.ch).
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"Complete genome sequence of spirochete.";
Science 281:375-388(1998).
-i- FUNCTION: Molecular cha
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                               MEDLINE-98332770; PubMed-9665876; Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J. Sodergren E., Hardham J.M., McLeod M.P., Chidambaram M., Utterback Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback McDonald L., Artiach P., Bowman C., Cotton M.D., Fujli C., Garlan Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.
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SMART; SM00387; HATPase_c; 1
PROSITE; PS00298; HSP90; 1.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Bacteria; Spirochaetes;
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                                                                                            similarity).
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By
SIMILARITY: BELONGS TO THE HEAT SHOCK
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1 333 A; SUBSTRATE-BINDING (BY
334 542 B (BY SIMILARITY).
543 616 C.
616 AA; 71218 MW; D676552F48DBEE84 CRC64
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Pred. No. 0.61
94; Mismatches
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mith H.O.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20150907; PubMed=10688199;
Lemieux C., Otis C., Turmel M.;
Pancestral chloroplast genome in Mesostigma viride branch of green plant evolution.";
Nature 403:649-652(2000).
-i- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NAD(P)H-quinone oxidoreductase chain J, chloroplast (EC 1.6.5.-)
(NAD(P)H dehydrogenase, chain J) (NADH-plastoquinone oxidoreductase
                                                                                                ProDom; PD001581; Complex1_30K; 1. PROSITE; PS00542; COMPLEX1_30K; 1. Oxidoreductase; NAD; NADP; Quinone
                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae; Mesostigmatales; Mesostigmataceae; Mesostigma.
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                                                                                                                                                                                 Pfam; PF00329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesostigma viride.
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                                                                                                                                                                                                        interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE COMPLEX I 30 kDa SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plastoquinol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFVFNVFCAKDRKTYDIFNEECV 202
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                                                                                                                                                                            IPR001268; Complex1_30K. 0329; complex1_30Kd; 1.
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                                                                         NADP; Quinone; Plastoquinone; Chl
20329 MW; 122ABFA9188D47B7 CRC64;
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Pred. No. 2.
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97.5;
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                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                           Chaperone;
                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00775; HEATSHOCK90.
SMART; SM00387; HATPase_C; 1.
PROSITE; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02518; HATPase_c; 1. Pfam; PF00183; HSP90; 2.
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InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR001404; Hsp90.
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PIR; F97862;
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 293:2093-2098(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21442074; PubMed=11557893;
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Rickettsiaceae; Rickettsieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTPG OR RC1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mechanisms of evolution in Rickettsia
                                                 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE008676; AAL03840.1;
97862; F97862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161
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                                                                                                                                                                      Similarity
DTGSWGSQFKCLQVQEIERKEEDYTVTSVFTF----
                                                                                            FVSAALATQAETTSAKAGENP--LWAHEELLGKY--QDAWKSIDQGVSVTYVLAKTTYEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPQEVCIK----VFVPRTKPIIPSVFWIWKTADFQERESYDMFG--IYYEGHPHL
                                                 YSSFMVADKVTVTSRKAGEDKVHIW-ESDGLGEYTVSDSDKEFTRGTEIVLHIKK---EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGCELWVKKSHYKHVPDYCTFVFNVFCA----KDRKTYDIFNEECVYNGEPWL
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                                                                                                                                                                                                                                                                                       ATP-binding; Heat shock; Complete proteome 1 328 A; SUBSTRATE-BINDING (BY 329 544 B (BY SIMILARITY).
                                                                                                                                                                                                                                            621 AA;
                                                                                                                                                                                                                                                                     545
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular chaperone. Has ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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41, Last sequence update)
41, Last annotation update)
htpG (Heat shock protein htpG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Renesto-Audiffren P., Fo
Cossart P., Weissenbach
                                                                                                                                                                                                                                            70804 MW;
                                                                                                                                                                      8.6%;
21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alphaproteobacteria; eae; Rickettsia.
                                                                                                                                                46;
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                                                                                                                                                                                             Score 96.5;
                                                                                                                                                                                                                                                                     C. B.
                                                                                                                                                                      Pred. No.
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                                                                                                                                             Mismatches
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                                                                                                                                                                                             DВ
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ch J., Claverie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.,
                                                                                                                                             81;
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                                                                                                                                                                                             Length 621;
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    RNASSPIKYYNVTETVKAV 117
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                                                                                                                                                                                                                                                                                                                    SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barbe V.,
                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
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HBPM_RHIAP
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Best Local
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MO1. Cell 3:661-671(1999).

1- FUNCTION: BINDS HISTAMINE WITH I
OUTCOMPETE HISTAMINE RECEPTORS 3
SUPPRESS INFLAMMATION DURING BIX

-i- SUBCELLULAR LOCATION: Secreted.
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                         use by non-profit institutions as long a
modified and this statement is not removed:
entitles requires a license agreement (See I
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        MEDLINE-99288454; PubMed-10360182; Paesen G.C., Adams P.L., Harlos K., Nuttall P.A., Stur Paesen G.C., Adams p.L., Harlos K., Nuttall P.A., Stur Paesen G.C., Adams p.L., Harlos K., Nuttall P.A., Stur Paesen G.C., Adams P.L., Harlos K., Nuttall P.A., Stur Paesen G.C., Nuttall P.A., Nuttall P.A.
                                                                                               the
                                                                                                                                                                                                                                                                                                  TISSUE-Salivary gland;
MEDLINE-99288454; Pubm
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HBPM_RHIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Emeropean Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
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21464 MW;
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36.0%;
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Pred. No. 8.
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INDICATES THAT I
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                                                             Usage
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                                                                                                                                                                                                  ITS FUNCTION :
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d three-
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                                                                                                                 a collaboration -
MBL outstation -
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Best Local
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SEQUENCE
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SIGNAL
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                                                                                                                                                                                               dimensional structure.";

MOL. Cell 3:661-671(1999).

- FUNCTION: BINDS HISTAMINE WITH A HIGH-AFFINITY.

- OUTCOMPETE HISTAMINE RECEPTORS INDICATES THAT IT SUPPRESS INFLAMMATION DURING BLOOD FEEDING.

- I- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Femmale-specific histamine-binding protein 1 precursor (F
Rhipicephalus appendiculatus (Brown ear tick).
Eukaryota; Metasoa; Arthropoda; Chelicerata; Arachnida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002970; His_binding,
Pfam; PF02098; His_binding; 1.
ProDom; PD152455; His_binding; 1.
                                  InterPro; IPR002970; His_binding. Pfam; PF02098; His_binding; 1.
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                      TISSUE=Salivary gland;
MEDLINE=99288454; PubMed=10360182;
Paesen G.C., Adams P.L., Harlos K.,
"Tick histamine-binding proteins: 1:
dimensional structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HBP1_RHIAP
077420;
                                                          EMBL; U96080; AAC63106.1;
HSSP; 077421; 1QFT.
                                                                                                  or send
                                                                                                             modified and entities requ
                                                                                                                                      use
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=34631;
                                                                                                                                                                                                                                                                                                                                                                      Parasitiformes; Ixodida;
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4; Mismatches
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ProDom;

PD152455;

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on: August 4, 2003, 17:13:07; Search time 24 Seconds (without alignments) 409.524 Million cell updates/sec

Title:
Perfect score:
Sequence: DRET6
1125
1 MKMQVVLLLIFVSAALATQA......DRKTYDIFNEECVYNGEPWL 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| u<br>u             | 32                 | 31  | 30                 | 29                 | 28         | 27                 | 26                 | 25        | 24         | 23        | 22        | 21                 | 20         | 19         | 18         | 17         | 16                 | 15         | 14         | 13         | 12         | 11         | 10         | 9          | 80         | 7          | 6          | 5          | 4          | ω          | 2          | _          | No.         | Result |
|--------------------|--------------------|---|--------------------|--------------------|------------|--------------------|--------------------|-----------|------------|-----------|-----------|--------------------|------------|------------|------------|------------|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-------------|--------|
| 75                 | 75                 | 75  | 75                 | 75.5               | 76         | 76                 | 76                 | 76        | 76.5       | 76.5      | 77        | 77                 | 78         | 78.5       | 79.5       | 79.5       | 80.5               | 81         | 81.5       | 82         | 82         | 82.5       | 84.5       | 85         | 86         | 87         | 96         | 96.5       | 97.5       | 252        | 265        | 290.5      | Score       |        |
| 6.7                | 6.7                | 6.7   | 6.7                | 6.7                | 6.8        |                    | •                  | •         |            |           | 6.8       | 6.8                | 6.9        | 7.0        | 7.1        | 7.1        | 7.2                | 7.2        | 7.2        | 7.3        | 7.3        | 7.3        | 7.5        | 7.6        | 7.6        | 7.7        | 8.5        | 8.6        | 8.7        | 22.4       | 23.6       | 25.8       | Match       |        |
| 647                | 626                | 424   | 414                | 1489               | 1068       | 1066               | 1031               | 260       | 724        | 393       | 909       | 523                | 215        | 864        | 629        | 621        | 621                | 700        | 627        | 637        | 381        | 318        | 621        | 656        | 2778       | 639        | 616        | 621        | 174        | 190        | 200        | 190        | Length      |        |
| <b>_</b>           | 1                  | <u>, , , , , , , , , , , , , , , , , , , </u> | _                  | -                  | <b>F-4</b> | -                  | H                  | -         | ш          | ب         | _         | Н                  | Н          | _          | <b>—</b>   | Н          | ب                  | ۲          | ب          | L          | <u> </u>   | ۳          | ۳          | ۲          | ۳          | _          | ۲          | ب          | Н          | Ь          | Н          | Ц          | B           |        |
| HTPG_MYCTU         | HTPG_BUCBP         | PORA_CAMJE                                    | Y878_METJA         | RNG2_SCHPO         | TRI_SULSO  | HYSA_STRPN         | YDG9_SCHPO         | DCK_MOUSE | DDX4_HUMAN | IDH_STRMU | HEX_ADEM1 | CP5C_CANMA         | NO22_SOYBN | YG3M_YEAST | HTPG_CHLTE | HTPG_HELPY | HTPG_HELPJ         | HS9C_DICDI | DNAK_RICPR | TRG5_ECOLI | RIR2_CAEEL | Y692_METTH | HTPG_RICPR | HTPG_MYCLE | FAF_DROME  | HTPG_TREPA | HTPG_BORBU | HTPG_RICCN | NUGC_MESVI | HBP1_RHIAP | HBPM_RHIAP | HBP2_RHIAP | ID          |        |
| Q50667 mycobacteri | Q89a93 buchnera ap | P80672 campylobact                            | Q58288 methanococc | 014188 schizosacch |            | Q54873 streptococc | Q10496 schizosacch |           |            |           |           | P16496 candida mal |            | -          |            |            | Q9zmm2 helicobacte |            | -          |            | -          |            |            |            | drosophila | -          |            |            |            |            |            | piceph     | Description |        |

| 45         | 44         | 43         | 42         | 41         | 40        | 39          | 38         | 37         | 36         | <u>3</u> 5 | 34          |
|------------|------------|------------|------------|------------|-----------|-------------|------------|------------|------------|------------|-------------|
| 73.5       | 73.5       | 73.5       | 74         | 74         | 74        | 74.5        | 74.5       | 74.5       | 74.5       | 74.5       | 75          |
| 6.5        | 6.5        | 6.5        | 6.6        | 6.<br>6    | 6.6       | 6.6         | 6.<br>6    | 6.<br>6    | 6.<br>6    | 6.6        | 6.7         |
| 2896       | 553        | 355        | 912        | 854        | 406       | 2768        | 890        | 726        | 492        | 400        | 3951        |
| L          | ب          | ۳          | $\vdash$   | ب          | ب         | Н           | Н          | -          | H          | -          | ۲           |
| HCYG_OCTDO | GKP2_HUMAN | UBPC_HUMAN | TBP1_HAEIN | TRIC_SULTO | IDH_SPHYA | THYG_HUMAN  | LPN1_HUMAN | NFI1_YEAST | YGCE_ECOLI | GTR3_RABIT | VGF1_IBVB   |
|            |            |            |            |            |           | P01266      |            |            |            |            | P27920      |
| octopus    | homo sap   | homo sapi  | haemophil  | sulfolobu  | sphingomo | homo sapien | homo sapi  | saccharom  | escherich  | oryctolag  | avian infec |

## ALIGNMENTS

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| EMBL; U96081; AAC63107.1; - PDB; 1QFT; 19-APR-00. PDB; 1QFY; 19-APR-00. InterPro; IPR002970; His_binding; ProDom; PD152455; | des wis   |  | LIT 1  RHIAP RHBP2_RHIAP 077421; 30-MAY-2000 30-MAY-2000 28-FEB-2003 Female speci Rhipicephalu Bukaryota a Parasitiform MCBI_TaxID=3        |
| 5081; AAC6310<br>T; 19-APR-00.<br>V; 19-APR-00.<br>; IPR002970;<br>02098; His_bi<br>PD152455; His<br>3D-structure.<br>19 20 19<br>20 19<br>31 31 36 44<br>48 48 55<br>57 56<br>66 66 66   | the Swiss I the Swiss I the Swiss I wan Bioinfo non-profit and this strequires a n email to   | FROM N.A., AND slivary gland; 9288454; PubMed C., Adams P.L., stamine-binding nal structure."; 13:661-671(1999) TON: BINDS HISTAMINE BESS INFLAMMATIC BLULAR LOCATION  | STAN<br>(Rel. 3<br>(Rel. 4<br>(Rel. 4<br>fic his<br>is apper<br>letazoa;<br>ixc<br>les; ixc   |
| nd 1  | ry is col<br>Institute<br>Ormatics<br>institute<br>institute<br>License<br>license  | ENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY UDE-Salivary gland; INE-99288454; PubMed-10360182; en G.C., Adams P.L., Harlos K., Nuttall P. & histamine-binding proteins: isolation, consional structure. *, Cell 3:661-671(1999).  Cell 3:661-671(1999).  TUNCTION: BINDS HISTAMINE WITH A HIGH-AFFI OUTCOMPETE HISTAMINE RECEPTORS INDICATES TO SUPPRESS INFLAMMATION DURING BLOOD FEEDING SUBCELLULAR LOCATION: Secreted. | STANDARD;  1. 39, Created) 1. 39, Last seq) 1. 41, Last ann histamine-bind ppendiculatus (ppendiculatus (azoa; Arthropoda Ixodida; Ixodida; |
| ng.<br>1.<br>EMALE-   | pyright. It is of Bioinforma Institute. Thatitude as long is not removed agreement (See also sib.ch).   | ST ST  | pRT; 190 A ted) sequence update annotation upda binding protein s (Brown ear ti poda; Chelicerat kodidae; Rhipice                           |
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| 324                | 165                 | 265  | 141 | 210  | 81  |
| 324 LMEMATYGHV 334 | 165 LAVKKSHYKHV 175 | 265 TLIVDPDGKGLDSHWQKTAFALLVGVILHALYKAKDDGGTATLPSVDAMLADPNRDIG-E 323 |     | 210KGELWALTAGWROKHAKNKVLRFEPASTSGGVCWNPLDEIRLGTEYEVGDVQNLA 264 | 81 QEIERKEEDYTVTSVETFRNASSPIKYYNVTETVKAVFQYGYKNIRNAIEYQVGGGLNIT 140 |
| •                  |                     | 23   | 4   | 54   | 0   |

Search completed: August 4, 2003, 17:15:58 Job time: 42 secs

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Page 6

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RESULT 14
T08530
Trag protein - Enterobacter aerogenes plasmid R751
C;Species: Enterobacter aerogenes
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: T08530
R;Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
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A;Cross-references: GB:AE002119; GB:AF222894; NID:96899153; PIDN:AAF30605.1; GSPDB:GN001
A;Experimental source: serovar 3; blovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical UU198 [imported] - Ureaplasma urealyticum C;SpecLes: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change ;C;Accession: D82922
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A:Introns: 18/3; 137/3; 256/2
C:Superfamily: herpesvirus ribonucleoside-diphosphate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of A;Reference number: A82870
A;Accession: D82922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, submitted to GenBank, February 2000
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A;Molecule type: DNA
A;Residues: 1-381 <WIL>
A;Cross-references: EMBL:Z35637; PIDN:CAA84688.1; GSPDB:GN00021; CESP:C03C10.3
A;Experimental source: Clone C03C10
C;Genetics:
C;Genetics:
A;Gene: CESP:C03C10.3
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DNA Seq. 1, 303-327, 1991
A; Title: Nucleotide sequence and
A; Reference number: S22992; MUID:
A; Accession: S22992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           traG protein - Escherichia coli plasmid R751 C;Species: Escherichia coli C;Date: 31-Dec-1993 #sequence_revision 02-Au:C;Accession: S22992; S42274
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                                                                                                                                                                                                    A; Genome: plasmid
                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X54458;
                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-628, 'D', 630-637 <LAN>
                                                                                                                                                                                                                                                                                                       A; Accession:
                                                                                                                                                                                                                                                                                                                       A; Reference number: S42274
                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library,
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A;Genome: pla
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                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-637 <ZIE>
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A; Residues: 1-637 <THO>
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16; Conservative
PTATGVYVGGWQDKDGNFFYLRHSGPEHVLTYAPTRSGKGVGLVVPTLLSWGASSVITDL
                              --LLGKYQDAWKSID------QGVSVTYVLAKTTYENDTG-----SWGSQFKCLQV 80
                                                                                                 VVLLLTFVSAALATQAETTSAKAGE----NPLWAHEE-----
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                                                                 LVSTVGLLGVAVAKVVTSNSSKANEYLHGSARWAEKKDIQAAGLLPRERNVLEIVTGKAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           e and organization of genes flanking the transfer origin MUID:92190548; PMID:1665997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strack, B.; Balzer, D.; Kroeger,
                                                                                                                                 30;
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                                                                                                                                                                                                                                                     NID: 942656; PIDN: CAA38327.1; PID: 942657
                                                                                                                                                    Score 82;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                        August 1990
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25;
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A; Experimental:
C; Genetics:
A; Gene: yomI
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C69192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stomatin-like protein - Methanobacterium thermoautotrophicum C:Species: Methanobacterium thermoautotrophicum
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A; Residues: 1-318 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A;Reference number: A69000; MUID:98037514; PMID:9371463 A;Accession: C69192
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38; Conserv
                                                                                                                                                                                                                                                         NIRNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNADQGCELW 166
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                                                                                                                                                                                                                                                                                                                                    ENDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIK-YYNVTETVKAVFQYGYK 123
                                                                                                                                                                                                                                                                                                                                                                                                              VVLLLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKDELKQYKQIADYND-----KGRPKWDLIADDDDY
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                                                                                                                                                                                                                     NLRNII-----GDLELDQTL--TSREMINTQLREVLDEATDKW 148
                                                                                                                                                                                                                                                                                                                                                                        VLLVLAFKSLKILRPYEKGVV------ERLGKYQ---RTVESGLVVIIPFIEAIK 55
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Pred. No. 1.1e+02;
?7; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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                                          K.S.; Zeng, Q.; Gibson,
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                                            Lee
hypothetical protein CO3C10.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te) C;Accession: T18876
R;Berks, M. submitted to the EMBL Data Library, August 1994
A;Accession: T18876
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C; Genet:
A; Note:
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A; Residues: 1-360 <GRA>
A; Cross-references: EMBL: U42580; NID: 94028896;
A; Experimental source: specific host Chlorella
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: T17996
R; Graves, M. V.; Van Etten,
submitted to the EMBL Data
A; Reference number: Z18806
A; Accession: T17996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein A494R - Chlorella C;Species: Chlorella virus PBCV-1 C;Date: 15-Oct-1999 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: C97308 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-163 <KUR>
RESULT 12
T18876
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Best Local
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37; Conserv
                                                                                                                                                                                                                                                               Similarity 25.8
41; Conservative
                                                                                              DTLIFTDGELCDVFYVPNADQGCELWVKKSHYKHVPDYC 179
                                                                                                                                                                VTSVFTFRNASSP-IKYYNVTETV-----KAVFQYGYKNIR-NAIE---YQVGGGLNIT 140
                                                                                                                                                                                                HEAVNGNIQLFQEKKMKLENGVN-----TKKTEE------KIKQIEEDEINYL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNAIEYQVGGGL-----NITDTLIFTDGELCDVFYVPNADQG-----CELWVKKSHY
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                                                                                                                                                                                                                                 HEELLGK---YQDAWKSIDQGVSVTYVLAKTTYENDTGSWGSQFKCLQVQEIERKEEDYT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHVPDYCTFVFNVFCAKD-RKTYDIFNEECV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEAAQIPVGEQLGIYSYKNITDIGIGLNPNLC-----
                                                                TLDAVTDRETVDQIYTCTCGGQMELWVNSTQSDLVCNEC
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                                                                                                                                                                                                                                                                               7.3%;
                                                                                                                                 ---PFIKEYDVKETVSDVTEQNSVFQVKSKNTHTNTFRKYLFHVEKVSNPT
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Library,
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                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                               ; Score 82; DB
; Pred. No. 12;
19; Mismatches
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Pred. No. 4.2;
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strain NC64A
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ATCC824
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15-Oct-1999 #text\_change

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C; Genetics:
A; Gene: htpG; RP840
C; Superfamily: heat sho
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A;Molecule type: DNA
A;Residues: 1-656 <STO>
A;Cross references: GB:AL450380; NID:gl3093407; PIDN:CAC30574.1; GSPDB:GN00147
C;Genetics:
A;Gene: htpG
C;Superfamily: heat shock protein 90
                                                                                                                                                                                                                                                                                                                                             80
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A; Residues: 1-621 < AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: H71645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: H71645
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.;
Nature 396, 133-140, 1998
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                                                                                                                                                                                                   GYKNIRNAIEYQVG---
                                                                                                                                                                                                                                                                           NDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYYNV----TETVKAVFQY 120
                                                                                                                                                                                                                                                                                                                                 FVSAALATQAETTSAKAGENPLWAHE-ELLGKY--QDAWKSIDQGVSVTYVLAK--TTYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSSFMVANKVELLTRKAGETAATRWSSD---GEATYTIESVDEAPQGTSVTLHLKPEDFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVSAALATQAETTSAKAGENPL--WAHEELLGKYQDAWKSID---QGVSVTYVLAKTTYE
                                                                                                                            ----SHYKHVPDYCTFVFNVFCAKD 190
                                                                                                                                                               QYKEFYKSLSYAVDDPWVTLHNKNEGAIEFTNLLFIPSSKTFDLFH-PDRKKRVKLYIKR
                                                                                                                                                                                                                                       DH------FRLKHIVKSYSDHIAVPIYFCDEAGNNEIQLNSASALWTRPKSEITED
                                                                                                                                                                                                                                                                                                             YSSFMVADKVTVTSRKAGESKVHTWESDGLGEYIVADSEQEFTRGTEIVLYIKKSETTFL
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[imported] - Listeria monocytogenes (strain EGD-e)
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Pred.
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Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                   --GGLNITDTLIFTDGELCDVFYVPNADQGCELWVKK 169
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A; NCCESSANDER A; NCCESSANDER A; NO LECULE type: DNA A; Rosidues: 1-917 <GLA>A; Cross-references: GB.NC_003210; A; Cross-
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-
C;Accession: AF1394
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Am.; Dominguez-Bernal, G.; Duchaud, E.; Durand,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 294, 849,852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez: A; Title: Comparative genomics of Listeria species. A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AF1394
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Best Local
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37; Conserv
REAKTSGGTIWYQFSIGG-----KTIGWVDSKALNTFYTPSMEK 363
                                                                                                                                                           KYKAMQV-NYEKIEYDKAITAYSRVKTATGNSVWTKPNKTEGAKLVNPLSSYSGKNLRII 324
                                                                                                                                                                                                                                        QFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYY--NVTETVKAV---FQYGYKNIR-- 126
                                                                                                                                                                                                                                                                                                                               GKGTVWSHD----
                                                                                                                                                                                                                                                                                                                                                                                                            GENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYENDT---GSWG-----S
                                                                         -----NAIEYO--VGGGLNITDTLIFTDGELCDVFYVPNADQ
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:CAD00636.1;
                                                                                                                                                                                                                                                                                                                               ----AVTRYLGGTTHTDPVAYFNQWGYNFNNFVSLINE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F.; Kurapkat, G.; Madueno, rrez, A.; Vazquez-Boland, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.; Baquero, I
Dussurget, O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
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.A.; Voss, H.; W
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itian, K.D.;
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Fsihi,
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Wehla
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probable transglycosylase - Bacillus subtilis phage SPBC2
C;Species: Bacillus subtilis phage SPBC2
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 15-Oct-1999

C; Accession: T12796; A69911

A;Description: The complete nucleotide A;Reference number: 217583
A;Accession: T12796 R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, submitted to the EMBL Data Library, August 1997 sequence of the Bacillus subtilis SPbetac2

pro

A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA
A; Residues: 1-2285 < LAZ>
A; Residues: 1-2285 < LAZ>
A; Cross-references: EMBL: AF020713; NID: g3025478; PID: g3025510; PIDN: AAC13005.1
R; Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.;
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.P.
C.; Bron, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrar

C.; Bron, S.; Ērouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
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Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
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Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
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A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A;Reference number: A69580; MUID:98044033; PMID:9384377

A; Accession: A69911

A; Status: nucleic acid sequence not shown; translation not

A; Molecule type: DNA A; Residues: 1-2285 <

Cross-references: GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB14053.1; PID:e11835

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A; Title: Complete genome sequence of Treponema pallidum, the complete genome sequence of Treponema pallidum the complete genome sequence of the complete genome sequence of the complete genome sequenc
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F71258

probable heat shock protein 90 (htpG) - syphilis spirochete
probable heat shock protein 90 (htpG) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-650 <KLE>
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C;Superfamily: heat shock protein
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A;Title: Conservation of gene arrangement and an unusual organization of rRNA genes A;Reference number: I40241; MUID:95111614; PMID:7812434
                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE001265; GB:AE000520; A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-639 <COL>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-639 <COL>
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A; Residues: 531-609 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: TP0984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770; PMID:9665876
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Best Local :
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                                                                                                                                                                                                                                        50;
                                                                                                                                                                                                                                                                        Similarity
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VTYVLAKTTYENDTGSWGSQFKCLQVQEIERKEEDY----TVTSVFTFRNASSPIKYYN 109
                                                                                VVLHLSQENSEFATR------WRLEEVIKKYSDHIAFPIYLHYLQKEYDKDGA 228
                                                                                                                                                    VVLLLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQD------AWKSIDQGVS
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                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                Score 87;
Pred. No.
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| <b>р</b> у    | ру  | ОУ   | Qy   | Query M<br>Best Lo<br>Matches  | A;Status: p A;Molecule A;Residues: A;Cross-ref A;Note: seq C;Keywords:   | A; Access A; Status A; Molecu A; Residu A; Cross• A; Note: A; Note: A; Access  | R;Fische<br>Developm<br>A;Title;<br>A;Refere<br>A;Conten   | RESULT 4<br>B49132<br>fat face<br>C;Specie<br>C;Date:<br>C;Access   | Qу<br>Db   | рb     | Qy   | Db |
|---------------|---|--|--|--|--|--|--|---|--|--------|--|----|
| 168 KKSHYKHVP | 111 TETVKAVFQYGYKNIRNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNADQGCELMV 167<br> | 53 VSVTYVLÄKTTYENDTGSWGSOFKCLOVQEIERKEEDVTVTSVFTFRNASSPIKYYNV 110  1 | 6 VILLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQDAWKSIDQG 52 | Match 7.6%; Score 86; DB 2; Length 2747;<br>Local Similarity 22.9%; Pred. No. 75;<br>Les 54; Conservative 28; Mismatches 72; Indels 82; Gaps 12; | A; Status: preliminary A; Molecule type: nucleic acid A; Molecule type: nucleic acid A; Molecule type: nucleic acid A; Residues: 1-2704, 'VT', 2707, 'ANNV' <fi2> A; Cross-references: GB:L04958; NID:g157410; PIDN:AAF01346.1; PID:g6013475 A; Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:1290 A; Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:1290 C; Keywords: alternative splicing</fi2> | A;Accession: B49132 A;Actaus: preliminary A;Cataus: preliminary A;Rolecule type: nucleic acid A;Residues: 1-2747 <fis> A;Cross-references: GB:L04959; NID:g157411; PIDN:AAF01345.1; PID:g6013474 A;Cross-references: GB:L04959; NID:g157411; PIDN:AAF01345.1; PID:g6013474 A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:1278 A;Accession: A49132</fis> | R;F1scher-Vize, J.A.; Rubin, G.M.; Lehmann, R. Development 116, 985-1000, 1992 A;Title: The fat facets gene is required for Drosophila eye and embryo development. A;Reference number: A49132; MUID:93202020; PMID:1295747 A;Contents: 180genic st | RESULT 4 B49132 fat facets (faf) splice form 1 - fruit fly (Drosophila melanogaster) fat facets: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 01-Dec-2000 C;Accession: B49132; A49132 | 160 DQGCELWYKKSHYKHYPDYCTEVENVFCAKD 190       : :  : | 278 TK | 110 VTETVKAVFQYGYKNIRNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNA 159 |    |

heat shock protein Hsp90 family [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10 C;Accession: A87112 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Davies, R.M.; Devili, K.; Duthoy, S.; Feltwell, T.; Fraser, A. eam, M.A.; Rutherford, K.M. acm, M.A.; Rutherford, K.M. Nature 409, 1007-1011, 2001 A;Authors: Ruther, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skeltc A;Authors: Ruther, S.; Seeger, K.; Simon, S.; Simonds, M.; Skeltc A;Authors and Sive gene decay in the leprosy bacillus. A;Reference number: A86909; MUID:21128732; PMID:11234002 A;Accession: A87112 20-Apr-2001 #text\_change 10-May-2001 Thomson, N.R.; Wheeler, Fraser, A.; Hamlin, N.; Skelton, J.; Squares,

P.R.; Holro

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#### Result No. Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database Maximum Minimum Total number of hits satisfying chosen parameters: Scoring table: Sequence: Title: Perfect score: OM protein - protein search, using sw model on: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. DB DB Score seq length: 0 length: 2000000000 PIR\_76:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Query Match BLOSUM62 Gapop 10.0 , 283308 seqs, 96168682 residues 1 MKMQVVLLLTFVSAALATQA......DRKTYDIFNEECVYNGEPWL August 4, 2003, 17:13:11; Search time 40 Seconds GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Length DB 163 380 381 390 637 627 621 725 455 865 1871 215 215 223 331 621 639 2747 656 621 917 2285 Gapext 0 F9786 G70169 G70169 G70169 F71258 B491132 B4911394 F71294 C69192 C97308 F117996 F1187996 F118799 F17996 F188792 F17999 Ħ SUMMARIES (without alignments) 502.481 Million cell updates/sec dnak-type molecula 90Kda chaperone chaperone and heat hypothetical prote hypothetical prote hypothetical prote nodulin-22 precurs cytochrome P450 52 hypothetical prote ribonuclease (EC 3 hypothetical prote probable periplasm probable heat shoc stomatin-like prot probable acetyltra hypothetical prote hypothetical prote conserved hypothet traG protein - Ent traG protein - Esc heat shock protein heat shock protein probable heat shoc fat facets (faf) s heat shock protein heat shock protein autolysin, amidase probable transglyc Description

| 45                                      | 44                 | 43                 | 42                 | 41                 | 40                 | 39                 | 38                 | 37                 | 36                 | 35<br>5            | 34                 | ω<br>ω             | 32                 | 31                 | 30                 |
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| 75.5                                    | 76                 | 76                 | 76                 | 76                 | 76                 | 76                 | 76                 | 76                 | 76                 | 76                 | 76.5               | 76.5               | 76.5               | 76.5               | 77                 |
| 6.7                                     | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                | 6.8                |
| 820                                     | 1277               | 1068               | 1066               | 1031               | 781                | 598                | 531                | 510                | 510                | 260                | 2819               | 807                | 635                | 587                | 914                |
| N                                       | N                  | N                  | N                  | Ν                  | N                  | Ν                  | N                  | N                  | N                  | N                  | N                  | N                  | ν                  | N                  | 2                  |
| D81382                                  | в84517             | S73091             | в95037             | T38411             | S49340             | AG0890             | T18741             | A64706             | A71816             | A55122             | A90551             | T18454             | T46407             | E87420             | S70906             |
| ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | hypothetical prote | hypothetical prote | hyaluronidase [imp | probable GTPase ac | heat-shock protein | probable arylsulfa | hypothetical prote | lipase-like protei | hypothetical prote | deoxycytidine kina | conserved hypothet | hypothetical prote | probable RNA helic | poly-beta-hydroxyb | transferrin-bindin |

# ALIGNMENTS

| Qу  | Qy<br>Db  | Qy  | Qy  | Query<br>Best<br>Match  | RESULT 1 F97862 heat shock p C; Species: R C; Date: 30-S C; Accession: R; Ogata, H.; Science 293, A; Title: Mec A; Reference A; Accession: A; Status: pr A; Molecule t A; Residues: A; Cross-refe C; Genetics: A; Gene: htpG C; Superfamil   |
|---|---|---|---|---|--|
| 170SHYKHVPDYCTFVFNVFCAKD 190<br>: :    :: <br>297 FISDENIDLIPSYLRFLRGVVDSED 321 | 118 FQYGYKNIRNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNADQGCELWVKK- 169<br>::   :   :   :   :   :   :   :   :   : | 67 DTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYYNVTETVKAV 117    :  :  :  :  :  :  :  :  :  :  :  :  : | 11 FVSAALATQAETTSAKAGENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYEN 66<br>:  :  :  :              :   :   :   : | Query Match 8.6%; Score 96.5; DB 2; Length 621;<br>Best Local Similarity 21.0%; Pred. No. 1.2;<br>Matches 43; Conservative 46; Mismatches 81; Indels 35; Gaps 10; | RESULT 1 F97862 C;Species: Rickettsia conorii C;Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C;Accession: F97862 R;Gqata, H; Audic, S; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2093-2098, 2001 A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893 A;Accession: F97862 A;Scatus: preliminary A;Molecule type: DNA A;Residues: 1-621 <kur> A;Cross-references: GB:AE006914; PIDN:AAL03840.1; PID:g15620441; GSPDB:GN00173 C;Genet: htpG C;Superfamily: heat shock protein 90</kur> |

RESULT 2
(70169)
(htpg) homolog - Lyme disease spirochete
heat shock protein 90 (htpg) homolog - Lyme disease spirochete
N; Alternate names: C62.5 heat shock protein
C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 20-Aug-1999
C; Accession: G70169; I40247
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.;
Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.

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Result
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US-09-815-242-10796

US-09-728-914-4

US-09-728-914-2

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4 US-10-043-344-5

5 US-10-043-344-5

5 US-10-043-344-9
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477.323 Million cell updates/sec
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Sequence 6, Appli
Sequence 6, Appli
Sequence 10796, A
Sequence 22, Appli
Sequence 22, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 17, Appli
Sequence 11, Appli
Sequence 9, Appli
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| 45               | 44               | 43                | 42                | 41  | 40                 | 39                | 38               | 37              | 36                 | 35<br>5   |                    |     | 32                 | 31                | 30           |                 |                   |      | 26                |                   | 24         |                   |                  |                   | 20                 |                   |             |        | 16                |
|------------------|------------------|-------------------|-------------------|-----|--------------------|-------------------|------------------|-----------------|--------------------|-----------|--------------------|-----|--------------------|-------------------|--------------|-----------------|-------------------|------|-------------------|-------------------|------------|-------------------|------------------|-------------------|--------------------|-------------------|-------------|--------|-------------------|
| 69.5             | 69.5             | 69.5              | 9.                | 9   | 70                 |                   |                  | 70              |                    | •         | 70.5               | •   | 70.5               | 71                | 71           | 71              | 71                | 71.5 | 71.5              | 71.5              | 71.5       | 71.5              | 72               | 72                | 72                 | •                 | 72.5        | 73     | 74.5              |
| 6.2              | 6.2              | 6.2               | 6.2               | 6.2 | 6.2                | 6.2               | 6.2              | 6.2             | 6.2                | 6.3       | 6.3                | 6.3 | 6.3                | 6. <sub>3</sub>   | ნ.<br>ა      | 6. <sub>3</sub> | ნ.<br>ა           | 6.4  | 6.4               | 6.4               | 6.4        | 6.4               | 6.4              | 6.4               | 6.4                |                   |             | 6<br>5 |                   |
| 374              | 374              | 373               | 373               | 225 | 853                | 638               | 576              | 576             | 247                | 470       | 470                | 451 | 451                | 677               | 619          | 618             | 550               | 2012 | 2012              | 924               | 891        | 564               | 956              | 956               | 507                | 2756              | 911         | 1417   | 990               |
| 15               | 15               | 14                | 1                 | H   | 15                 | 11                | 15               |                 | 10                 | 14        | 1                  | 14  | 11                 | 10                | 11           | 15              | 15                | 11   | 10                | 14                | 14         | 15                | 15               | 14                | 10                 | 15                | 15          | 10     | 14                |
| US-10-270-878-39 | US-10-270-875-39 | -10-042-431-      | -09-759-130E      | N   | US-10-156-761-8930 | 7                 | US-10-011-548-30 | US-09-731-175-4 | US-09-738-626-3674 | -10-042-4 | US-09-759-130B-439 | -10 | US-09-759-130B-413 | -09-862-027       | -09-934-455- | -403            | US-10-081-872-106 | 36   | 9-808-602         | US-10-028-056-5   | 0-028-056- | US-10-081-872-120 | US-10-093-037-63 | US-10-121-032-63  | US-09-738-626-5458 | US-10-331-061-7   | -10-043-344 | -09-   | US-10-028-056-3   |
| 39,              | e 39             | Sequence 6, Appli | Sequence 376, App | 11  | 89                 | Sequence 22, Appl | e 30,            | 4, Appl         | 367                | 69,       | 439,               | 43, | 413,               | Sequence 38, Appl | 142,         | 166,            | 106,              | 57,  | Sequence 68, Appl | Sequence 5, Appl1 | 4          | Sequence 120, App | 63               | Sequence 63, Appl | 54.5               | Sequence 7, Appli | e 107, Ap   | 78,    | Sequence 3, Appli |

### ALIGNMENTS

RESULT 1 US-10-085-572-7

Sequence 7, Application US/10085572 Publication No. US20020151499A1 GENERAL INFORMATION:

APPLICANT: Nuttall, Patricia, Ann
APPLICANT: Paesen, Guldo, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
FILE REFERENCE: 2488-1-003
CURRENT APPLICATION NUMBER: US/10/085,572
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/CB00/03282
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 9920674.0
PRIOR TILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

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; LENGTH: 171
; TYPE: PRT
; ORGANISM: FS-HBP;
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                                                          62 SIQAEFLEMNNADINMQF--ATEKVTAVKMYGY-NRENAFRYETEDGQVFTDVIAYSD-D 117
                                                                              91 TVTSVFTF-RNASSPIKYYNVTETVKAVFQYGYKNIRNAIEYQVGGGLNITDTLIFTDGE 149
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NCDVIYVPGTDGNEEGYELWT--TDYDNIPANCLNKFNEY-AVGRETRDVFTSACL
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; ORGANISM: MS-HBP
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; TYPE: PRT
; ORGANISM: FS-HBP 2
US-10-087-195-7
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Publication No. US20020193306A1
GENERAL INFORMATION:
APPLICANT: Nuttall, Patricia, Anne
APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Allergic Rhinitis
FILE REFERENCE: 2488-1-004
CURRENT FILING DATE: 2002-03-01
CURRENT FILING DATE: 2002-03-01
                                                                                        Matches
                                                                                                                                                                                                                                                                      SEQ ID NO 8
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Best Local :
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                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/GB00/03282
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 9920674.0
PRIOR FILING DATE: 1999-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nuttall, Patricia, Ann
APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/085,572 CURRENT FILING DATE: 2002-02-27
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PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/GB00/03287 PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0-087-195-7
                                                                                                                                                                                                                                                   LENGTH:
                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                  30 NPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYENDTGSWGSQFKCLQV--QEIERKE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SIQAEFLEMNNADTNMQF -- ATEKVTAVKMYGY - NRENAFRYETEDGQVFTDVIAYSD-D 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 PLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYENDTGSWGSQFKCLQVQEIERKEEDY 90
                                                                                                                                                                                                                                                 182
                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDP-VWGNDFTCVGVMANDVNEDEK 61
NPTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTD-GVWGEEFTCVSVTAEKIGKKK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCDVIYVPGTDGNEEGYELWT--TDYDNIPANCLNKFNEY-AVGRETRDVFTSACL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCDVFYVPNAD --- QGCELWVKKSHYKHVPDYCTFVFNVFCAKDRKTYDIFNEECV 202
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.1%; Score 282; DB 14; 37.5%; Pred. No. 7.3e-23;
                                                                                 22.4%; Score 251.5; DB 14; 35.3%; Pred. No. 1.7e-19; tive 29; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Mismatches
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                                                                                                                                Length 182;
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US-10-085-572-6
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                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10085572 Publication No. US20020151499A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/085,572
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/GB00/03282
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 9920674.0
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEO ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10087195 Publication No. US20020193306A1
                                                                                                                                                                                                                                                                                                                APPLICANT: Nuttall, Patricia, Ann
APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Conjunctivitis
FILE REFERENCE: 2488-1-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/GB00/03287
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 9920673.2
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CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Paesen, Guido, Christiaan
TITLE OF INVENTION: Treatment of Allergic Rhinitis
FILE REFERENCE: 2488-1-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nuttall, APPLICANT: Paesen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-09-01
                    ORGANISM: FS-HBP1
                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 FTDGELCDVFYVP---NADQG-CELWVKKSHYKHVPDYCTFVFNVFCAKDRKT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 FSDYKNCDVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 EDYTVTSVFTFRNAS-SPIKYYNVTETVKAVFQYGYKNIRNAIEYQVGGGLNIT--DTLI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 NPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYENDTGSWGSQFKCLQV--QEIERKE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 LNATI----LYKNKHLTDLKESHETITVWKAYDY---TTENGIKYETQGTRTQTFEDVFV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NPTWANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTD-GVWGEEFTCVSVTAEKIGKKK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSDYKNCDVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNATI----LYKNKHLTDLKESHETITVWKAYDY---TTENGIKYETQGTRTQTFEDVFV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTDGELCDVFYVP---NADQG-CELWVKKSHYKHVPDYCTFVFNVFCAKDRKT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDYTVTSVFTFRNAS-SPIKYYNVTETVKAVFQYGYKNIRNAIEYQVGGGLNIT--DTLI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Guido, Christiaan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.4%;
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Query Match

21.2%;

Score 239;

DB 14;

Length 172;

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US-09-815-242-10796
Sequence 10796, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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SEQ ID NO 6
LENGTH: 172
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                                                                                                                                                        APPLICANT:
APPLICANT:
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                   APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nuttall, Patricia, Anne
APPLICANT: Paesen, Guido, Christiaen
TITLE OF INVENTION: Treatment of Allergic Rhinitis
FILE REFERENCE: 2488-1-004
CURRENT APPLICATION NUMBER: US/10/087,195
CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/GB00/03287
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 9920673.2
                                                                                                                                                                                                                             APPLICANT:
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NUMBER OF SEQ ID NOS:
CURRENT APPLICATION NUMBER: US/09/815,242
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ORGANISM: FS-HBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 ELCDVFYVPNAD----QGCELWVKKSHYKHVPDYCTFVFNVFCAKDRKTYDIFNEECV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 DNCYVIYALGPDGSGAGYELWA--TDYTDVPASCLEKFNEYAA-GLPVRDVYTSDCL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 ELCDVFYVPNAD----OGCELWYKKSHYKHVPDYCTFVFNVFCAKDRKTYDIFNEECV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 DYTVTSVFTFRNASSPIKYYNVTETVKAVFQYGYKNIRNAIEYQVGGGLNITDTLIFTDG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 ENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYENDTGSWGSQFKCLQVQEIERKEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DNCYVIYALGPDGSGAGYELWA--TDYTDVPASCLEKFNEYAA-GLPVRDVYTSDCL
                                                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.2%; Score 239; DB 14; Length 172; 34.5%; Pred. No. 3.7e-18; ative 24; Mismatches 82; Indels 1
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24; Mismatches 82;
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                                                                                                                                                                                      ; ORGANISM: Ixodes scapularis US-09-728-914-4
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
Best Loc
Matches
                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
LENGTH: 221
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LENGTH: 722
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APPLICANT: DAS, SUBRATA
TITLE OF INVENTION: TICK ANTIGENS AND COMPOSITIONS AND METHODS COMPRISING
TITLE OF INVENTION: THEM
FILE REFERENCE: YU-107
FILE REFERENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/728,914
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 60/169,048
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/240,716
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEO ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 72
TYPE: PRT
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Local Similarity 23.
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8.7%; Score 97.5; DB 23.4%; Pred. No. 0.015; tive 43; Mismatches
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    Indels
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US-09-728-914-22
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             CURRENT APPLICATION NUMBER: US/09/932,183A CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/308,375
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US98/18828
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
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Patent No. US20020127641A1
GENERAL INFORMATION:
APPLICANT: Estell, David A.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394C1-US
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PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 39
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CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 60/169,048
PRIOR FILING DATE: 1999-12-03
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27; Conserv
   FastSEQ
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Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%; Score 84; DE 9; Length 217; 24.1%; Pred. No. 0.45;
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US-10-090-624-12
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LENGTH: 2285
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Best Local Similarity
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                     584 GATKITGDLTFDTSYNDLDLYLYDP 608
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SHIMOJO, Tomoko
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PRIOR APPLICATION NUMBER: 151969/1997
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/445,472
PRIOR FILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA=6
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ORGANISM: Bacillius subtilis
                                                                                                                                                                  496 YTAYYGFEK----VGYYNPTAGTWTVKVV---SYKGAAN---YQVDVVSDGSLSQSGGGN 545
                                                                                                                                                                                                                                                                          436 KYDDYAKLTFTGSVADKGSATHTFDVSGATFVTATLYWDTGSSDIDLYLYDPNGNEVDYS 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GY-----KNIRNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNADQGCELWVKK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  791 NKDSTDKLIQQYK-----ELQKVKESRSLTS-----DEEQEYLQVTQQLAQTFPALVK 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             743 LLVSTLVGGAFAALG------WALESLISSFAEAKKAKDDFEQSQQTNVEAITT 790
                                                                                                                                                                                                           92 VTSVFTFRNASSPIKYYNVTE---TVKAVFQYGYKNIRNAIEYQV----
                                                                                                                                                                                                                                                                                                                            41 KYQDAWK-----SIDQGVSV-TYVLAKTTYENDTGSW--GSQFKCLQVQEIERKEEDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 YENDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYYNVTETVKAVFQ---Y 120
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AKDRKTYDI ---- FNEECVYNGEP 207
                                                            PNPNPNPTPTTDTQTFT-GSVND--YWDTSD
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                                                                                                        -----LNITDTLIFTDGELCDVFYVPNADQGCELWVKKSHYKHVPDYCTFVFNVFC 187
                                                                                                                                                                                                                                                                                                                                                                                                      7.2%;
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23.3%;
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                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 81; DB 14; Length 659; Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 83; DB Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                               TETMNVNS
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; ORGANISM: Haemophilus influenzae US-10-043-344-11
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US-10-043-344-11
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; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-5
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Best Local !
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                                                                                   SEQ ID NO 11
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APPLICANT:
APPLICANT:
                                                                                                   CURRENT APPLICATION NUMBER: US/10/043,344
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 08/649,518
PRIOR FILING DATE: 1996-05-17
NUMBER OF SEQ ID NOS: 160
SOFTMARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                              APPLICANT: LOOSMORE, Sheena M. APPLICANT: Harkness, Robin E. APPLICANT: Schryvers, Anthony B. APPLICANT: Chong, Pele APPLICANT: Gray-Owen, Scott
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PRIOR FILING DATE: 1996-05-17
NUMBER OF SEO ID NOS: 160
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APPLICANT: Klein, Michel H.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
FILE REFERENCE: 1038-1221 MIS
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APPLICANT: K1611, MICHG1 H.
TITLE OF INVENTION: TRANSBERRIN RECEPTOR GENES
FILE REFERENCE: 1038-1221 MIS
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CURRENT FILING DATE: 2002-07-01
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                                         LENGTH: 914
TYPE: PRT
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Gray-Owen, Scott
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US-10-043-344-9
$\text{Sequence 9, Application US/10043344}$
$\text{Fpublication No. US20030088086A1}$
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US-10-043-344-7
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Best Local Similarity 23.0%;
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APPLICANT: Klein, Michel H.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
FILE REFERENCE: 1038-1221 MIS
CURRENT APPLICATION NUMBER: US/10/043,344
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 08/649,518
PRIOR APPLICATION NUMBER: 08/649,518
PRIOR FILING DATE: 1396-05-17
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APPLICANT:
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NUMBER OF SEQ ID NOS: 160
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                                                                                                                                                                                                                                                                                                                                           65 ENDTGS-----WGSQFKCLQVQEIERKEE-----DYTVTSVFTFRNASS 103
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                                                                                                                                                                   PNADQGCELWVKKSHYKHVPD--YCTFVFNVFCAKDRK 192
                                                                                                                             -----LW-----KRIPYGWYATFAYNQVKVKDQK 768
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Gray-Owen, Scott
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; Pred. No. 20;
24; Mismatches
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APPLICANT: LOOSMOTE, Sheena M.
APPLICANT: Harkness, Robin E.
APPLICANT: Schryvers, Anthony B.
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Murdin, Andrew D.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
FILE REFERENCE: 1038-1221 MIS
CURRENT APPLICATION NUMBER: US/10/043,344
CURRENT APPLICATION NUMBER: 08/649,518
PRIOR APPLICATION NUMBER: 08/649,51
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Search completed: August 4, 2003, 17:26:02 Job time: 53 secs
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                                                                                                                                                                                                     745 -----LW-----KRIPYGWYATFAYNQVKVKDQK 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 PIKYYNVTETVKAVFQ-----YGYKNIRNAIEYQVGGGLNITDTLIFTDGELCDVFYV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             647 RNPSFSEMYGWRYGGKNDEVYVGKFK----PETSRNQEFGLALKGDFGNIEISHFSNA-- 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 YVDLGLGIRYDVSRTKANESTI-----SVGKFKNFSWNTGIVIKPTEWLDLSYRLS-TGF 646
                                                                                                                                                                                                                                                                                                                   157 PNADQGCELWVKKSHYKHVPD--YCTFVFNVFCAKDRK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                       701 ---YRNLIAFAEELSKNGTGKGNYGYHNAQNAKLV----GVNITAQLDFNG------ 744
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-478-435-5
US-08-478-33-5
US-08-478-37-A-5
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US-08-637-654-5
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| 8.1%<br>20.8%<br>tive                                | on:  ON:  ON:  Michael  man, Lloyd  ION:  Protein  ION:  Platele  ADDRESS:  erck 6 Co., I  Box 2000  ersey  LE FORM:  Floppy disk  Floppy disk  Floppy disk  Floppy 100  ED NOS/  TENISTION:  TERISTICS:  amino acids  acid  unknown  protein  NINGOMANOWN  Sold   | 914<br>406 1<br>406 1<br>406 3<br>391 4<br>912 1<br>912 2<br>912 2<br>912 2<br>912 2<br>912 2<br>912 3   |
| ; Score 91; DB<br>; Pred. No. 0.00<br>33; Mismatches | 2A r Inh to Co 1.0, 1.0, 1.0, 1.0, 1.0, 1.0, 1.0, 1.0,   | US-08-649-518 US-08-977-771 US-09-361-773 US-09-107-532 US-09-107-532 US-09-107-532 US-08-487-890 US-08-487-890 US-08-478-435 US-08-478-373 US-08-478-373 US-08-474-671 US-08-483-577 US-08-483-577  |
| 1;<br>51;<br>82                                      | ing  | -518-11<br>-881-2<br>-771-2<br>-771-2<br>-532A-4419<br>-532A-5142<br>-632A-5142<br>-890A-9<br>-435-7<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-435-9<br>-4 |
| ength 202<br>Indels                                  | #1.25  | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0  |
| 60;  |  | Sequence   |
| Gaps   |  | 11, Appl<br>2, Appli<br>2, Appli<br>2, Appli<br>4419, Ap<br>6376, Ap<br>7, Appli<br>9, Appli<br>7, Appli<br>7, Appli<br>9, Appli<br>9, Appli<br>9, Appli<br>9, Appli<br>9, Appli<br>9, Appli<br>9, Appli   |
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                                                                                            Query Match
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GENERAL INFORMATION:
                                                                Matches
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                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5279:
                                                                            Госат
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                     FEATURE:
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                             26 KAGENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYEND--TGSWGSQFKCLQVQEI 83
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                                                                47;
                                                                            Similarity
 KFPEGFLWGGATAANQCEGAWDVDEKGLSVSDVY---TFDSDLPKEKWTDQWHMMTHQQV
                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                        TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                               NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
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COMPUTER: PC
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                                                                                                                                                                     NAME/KEY:
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Pred. No. 1
                                                              Mismatches
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AND AMINO ACID SEQUENCES RELATING TO
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LENGTH: 2285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                GENERAL INFORMATION:
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SOFTWARE: FastSEQ
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                                                                                                                                                    APPLICANT:
                                          NUMBER OF SEQUENCES: 4
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 STREET:
                               ADDRESSEE:
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Washington
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; LENGTH: 2285
TYPE: PRT
; ORGANISM: Bacillius subtilis
US-09-308-375-2
                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08894818B Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/308,375
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genencor International, Inc. TITLE OF INVENTION: Proteases From Gram-Positive Organisms
                                                                                           APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             791 NKDSTDKLIQQYK-----ELQKVKESRSLTS-----DEEQEYLQVTQQLAQTFPALVK
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419 Seventh Street N.W.,
                                                                                                                                                                                                                      MORISHITA, Mio
YAMAMOTO, Katsuhiko
                                                                                                                                                                   ASADA, Kiyozo
                                                                                                                                                                                          MITTA, Masanori
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                         Browdy and Neimark
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No. 16;
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RESULT 5
US-084-818B-5
; Sequence 5, Application US/08894818B
; Patent No. 6261812
; Patent No. 6261812
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                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                   APPLICANT:
                                       APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE
NUMBER OF SEQUENCES: 42
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                                CORRESPONDENCE ADDRESS
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TOPOLOGY: 11n
MOLECULE TYPE:
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FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 659 amino acids
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FILING DATE: 07-NOV-1996
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                ADDRESSEE:
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3: Browdy and Neimark 419 Seventh Street N.W.,
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                                                                                                                                                  MORISHITA, Mio
YAMAMOTO, Katsuhiko
                                                                                                                   MITTA, Masanori
ASADA, Kiyozo
                                                                                                                                                                                   TAKAKURA, Hikaru
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Ste.
                                                                   PROTEASE
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                                                                                                                                                                                                                                                     Sequence 12, Application US/09445472 Patent No. 6358726
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                                                                                                       APPLICANT: ASADA, Kłyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRPESSING
FILE REFERENCE: TAKAKURA-6
                                                                   CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
                                                                                                                                                                                               APPLICANT: TAKAKURA, Hikaru APPLICANT: MORISHITA, Mio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 737-35 INFORMATION FOR SEQ ID NO:
                              PRIOR FILING DATE: 1997-06-10
                                                                                                                                                                                  APPLICANT:
                 NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/C
FILING DATE: 07-NOV-1996
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LENGTH: 659 amino acids
TYPE: amino acid
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APPLICATION NUMBER: JP 3:
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: lir
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OPERATING SYSTEM: PC-DOS/MS-DOS
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1 Similarity 25.9%;
53; Conservation
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                 SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                   AKDRKTYDI----FNEECVYNGEP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                         PNPNPNPTPTTDTQTFT-GSVND--YWDTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LNITDTLIFTDGELCDVFYVPNADQGCELWVKKSHYKHVPDYCTFVFNVFC 187
                                                                                                                                                                              MORISHITA, Mio
SHIMOJO, Tomoko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        628-5197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP 323285/1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 81; DB 3; Length 659; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                              HYPERTHERMOSTABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
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Gaps

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RESULT 7
US-08-487-890A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 12
LENGTH: 659
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                   TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
TITLE OF I
 SEQUENCE CHARACTERISTICS:
                                                REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                   APPLICATION NUMBER: US 01 FILING DATE: 29-DEC-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/175,116
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                 FILING DATE: 08-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                          NAME: Stewart, Michael I REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/487,890A FILING DATE: 07-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Ontario
                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 GATKITGDLTFDTSYNDLDLYLYDP 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 PNPNPNPTPTTDTQTFT-GSVND--YWDTSD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 YTAYYGFEK----VGYYNPTAGTWTVKVV---SYKGAAN---YQVDVVSDGSLSQSGGGN 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 VTSVFTFRNASSPIKYYNVTE----TVKAVFQYGYKNIRNAIEYQV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 KYQDAWK-----SIDQGVSV-TYVLAKTTYENDTGSW--GSQFKCLQVQEIERKEEDYT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toronto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Sim & McBurney
6th Floor, 330 Un
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Yang, Yan-Ping
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                                    595-1163
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147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.2%; Score 81; DB 4; Length 659
25.9%; Pred. No. 4.2;
                                                                                                                                                                                      US 08/148,968
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                                                                                           1038-466 MIS: jb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: amino acid
; STRANDEDNESS: sin
; TOPOLOGY: linear
US-08-487-890A-5
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US-08-478-435-5
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GENERAL INFORMATION:
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 08-NOY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: US 08,
FILING DATE: 29-DEC-1993
                                                                                                                                                                                                                                                                                                                               COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                         FILING DATE: 29-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 08-NOV-
TELECOMMUNICATION INFORMATION:
                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                  NAME: Stewart, Michael REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 07-JUI
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CITY: Toronto
                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            593 YVDLGLGMRYDVSRTKANESTI-----SVGKFKNFSWNTGIVIKPTEWLDLSYRLS-TGF 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 EN------DTGSWGSQFKCLQVQEIERKEE------DYTVTSVFTFRNASS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNPSFAEMYGWRYGGKDTDVYIGKFK-'---PETSRNQEFGLALKGDFGNIEISHFSNA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suite 701,
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Klein, Michel
WENTION: Transferrin Receptor Genes
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Yang, Yan-Ping
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Harkness, Robin
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                                                                                            08-NOV-1993
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21.98;
                                                                                                                                                                US 08/175,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 University Avenue
                                                                                                          US 08/148,968
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                             24,973
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                 1038-462 MIS:vg
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Pred. No. 9.9;
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Best Local S
Matches 48
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                   NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Transferrin Receptor Genes NUMBER OF SEQUENCES: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                 Toronto
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Suite 701, 330 Unviersity Avenue
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Yang, Yan-Ping
Yandin, Andrew
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Klein, Michel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chong, Pele
                                                       (416) 595-1155
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21.9%; Pred. No. 9.9;
ative 32; Mismatches
                                                                                                                                                                                            US/08/337,483
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-337-483-5
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
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NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                         APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Transferrin Receptor Genes NUMBER OF SEQUENCES: 147
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                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/478,373 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           647 RNPSFAEMYGWRYGGKDTDVYIGKFK----PETSRNQEFGLALKGDFGNIEISHFSNA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ontario
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Suite 701, 330 University Avenue
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Klein, Michel
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Yang, Yan-Ping
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Harkness, Robin
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                                                                                                                                                                                      US 08/175,116
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Pred. No. 9.9;
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US-08-474-671-5
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Best Local Similarity 21.9%;
Matches 48; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                            ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rela
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
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TITLE OF IN
                                                                                       PRIOR APPLICATION DATA:
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                                                                                                        APPLICATION NUMBER: FILING DATE: 29-DE
                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                          APPLICATION NUMBER: US 08/148,968 FILING DATE: 08-NOV-1993
                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                        FILING DATE: 07-JUI
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Suite
CITY: Toronto
              REGISTRATION
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 VPNADQGCELWVKKSHYKHVPD--YCTFVFNVFCAKDRK 192
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                                                                                                                                                                                                                                                                                                                                                                                                  Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08474671
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Suite 701, 330 University Avenue
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Klein, Michel
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Chong, Pele
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Harkness, Robin
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Michael . 24,973
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                                                                                                                       US 08/175,116
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Pred. No. 9.9;
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US-08-483-577A-5
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                                                                                                                                                                                                         COUNTRY:
ZIP: M5G 1R7
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: FLOPSYMS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5,
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Best Local
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                             FILING DATE: 29-DEC-PRIOR APPLICATION DATA:
                                                                            APPLICATION NUMBER: US 08/337,483 FILING DATE: 08-NOV-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                 APPLICATION NUMBER: US/08/483,577A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                             STREET: Suite
CITY: Toronto
                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                       Suite 701, 330 Unviersity Avenue
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Klein, Michel
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Yang, Yan-Ping
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Harkness, Robin
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08-NOV-1993
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, 595-1163
- NO: 5:
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21.98;
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                                                                US 08/175,116
               US 08/148,968
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REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHAN: 1416) 595-1155
TELEPHAN: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-577A-5
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APPLICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/337,483
APPLICATION NUMBER: US 08/337,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.1%; Score 79.5; DB 3; Length 913; Best Local Similarity 21.9%; Pred. No. 9.9; Matches 48; Conservative 32; Mismatches 60; Indels 7
                                                                                                                                                                                                                                                                                                STREET: 6th Floor, 330 University Avenue CITY: Toronto STATE: Ontario COUNTRY: Canada ZIP: M5G 1R7
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,438
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APPLICANT:
TITLE OF IN
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 24,973
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Gray-Owen, Scott
Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
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Harkness, Robin
Schryvers, Anthony
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|---|----------|-----------------------|------------|---------------------------------|------------------------------|--------|----------------|---|--|----------|-------------|---------------------------|-------|--|------------------|---------------------------------|---|-----------------------------------|--|------|--|---|---|--|---|
| CATION NUMBER<br>G DATE: 05-A<br>IFICATION: 4 | Patentir | ER: IBM PC compatible | ER READABI | COUNTRY: Canada<br>ZIP: M5G 1R7 | CITY: TOPONTO STATE: Ontario | TREET: | PONDENCE ADDRE | TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES NUMBER OF SEQUENCES: 147 | APPLICANT: Murdin, Andrew D APPLICANT: Klein, Michel H | Yang, Ya | chong, Pele | Harkness, .<br>Schryvers, | ANT:  | Patentine of Appracation of Court of Patentine of Court o | 14<br>637-654-5  | 746LWKRIPYGWYATFAYNRVKVKDQK 769 | 156 VPNADQGCELWVKKSHYKHVPDYCTFVFNVFCAKDRK 192 | YRNLIAFAEELSKNGTTGKGNYGYHNAQNAKLV | 104 PIKYYNVTETVKAVFQYGYKNĮRNAIEYQVGGGLNITDTLIFTDGELCDVFY 155 |      | 65 ENDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASS 103 | 593 YVDLGLGMRYDVSRTKANESTISVGKFKNFSWNTGIVIKPTEWLDLSYRLS-TGF 646 | 11 FVSAALATQAETTSAKAGENPLWAHEELLGKYQD-AWKSIDQGVSVTYVLAKTTY 64 | Query Match 7.1%; Score 79.5; DB 3; Length 913;<br>Best Local Similarity 21.9%; Pred. No. 9.9;<br>Matches 48; Conservative 32; Mismatches 60; Indels 79; Gaps 13 | APPLICATION NUMBER: US 08/175,116 FILING DATE: 29-DEC-1993 PRIOR APPLICATION NUMBER: US 08/148,968 FILING DATE: 08-NOV-1993 ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I REGISTRATION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 1038-720 TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155 TELEPHONE: (416) 595-1163 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 913 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: single TOPOLOGY: linear |

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

PCT/CA94/00616

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RESULT 15
US-08-649-518-5
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: F1Dppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,518
FILING DATE: 17-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
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LENGTH: 913 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
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                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                             DDRESSEE:
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361779
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                                                                                                                                                                                                                                                                                         6th Floor, 330 Unviersity Avenue
                                                                                                                                                                                                                                      Canada
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Klein, Michel
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Yang, Yan-Ping
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                                                                                                                                                                                                                                                                                                             Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                        Andrew
                                                                                                                                                                                                                                                                                                                                               Transferrin Receptor Genes
160
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
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                                                                                    156 VPNADQGCELWVKKSHYKHVPD--YCTFVFNVFCAKDRK 192
                                                                                                                                                          104 PIKYYNVTETVKAVFQ-----YGYKNIRNAIEYQVGGGLNITDTLIFTDGELCDVFY 155
                                                                                                                                                                                              647 RNPSFAEMYGWRYGGKDTDVYIGKFK----PETSRNQEFGLALKGDFGNIEISHFSNA-- 700
                                                                                                                                                                                                                                                                    593 YVDLGLGMRYDVSRTKANESTI----SVGKFKNFSWNTGIVIKPTEWLDLSYRLS-TGF 646
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2003, 17:18:16
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Gaps

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Search completed: August Job time: 31 secs

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                                                                    SUMMARIES
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| Histacalin protein | AAB73261 | 22 |                          | 25.1  | 282   | 9        |
|--------------------|----------|----|--------------------------|-------|-------|----------|
| Histacalin protein | AAB74289 | 22 |                          | 25.1  | 282   | <b>6</b> |
| Histamine binding  | AAY18084 | 20 | 198                      | 25.3  | 284.5 | 7        |
| Histamine binding  | AAY18079 | 20 |                          | 25.8  | 290.5 | o        |
| Tick vasoactive am | AAW37447 | 19 |                          | 25.8  | 290.5 | ъ        |
| Histamine binding  | AAY18085 | 20 |                          | 31.4  | 353   | ۵        |
| Histamine binding  | AAY18086 | 20 |                          | 32.4  | 364   | ω        |
| Histamine binding  | AAY18081 | 20 |                          | 100.0 | 1125  | 2        |
| Tick vasoactive am | AAW37449 | 19 |                          | 100.0 | 1125  | 1        |
| Description        | ID       | BB | Query<br>Match Length DB | Query | Score | No.      |
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| -                  | ABG04465 | 22 | 716   | 7.0  | 79    | 5  |
|--------------------|----------|----|-------|------|-------|----|
|                    | AAY80353 | 21 | 913   | 7.1  | •     | 4  |
|                    | AAY51687 | 21 | 913   | 7.1  | •     | ω  |
| enz                | AAW53042 | 19 | 913   | 7.1  | 79.5  | 2  |
| Amino acid sequenc | AAW08957 | 18 | 913   | 7.1  | 79.5  | Ë  |
| _                  | AAR77884 | 16 | 913   | •    | 79.5  | ö  |
| _                  | AAW21012 | 18 | 638   |      | 80.5  | 9  |
| chapero            | AAW20536 | 18 | 597   | 7.2  | 80.5  | 8  |
| Sec                | AAW94840 | 20 | 659   | 7.2  | 81    | 37 |
| ccus prot          | AAW24121 | 18 | 659   | 7.2  | 81    | 8  |
|                    | AAW24123 | 18 | 659   | 7.2  | 81    | 5  |
| Drosophila melanog | ABB66456 | 22 | 876   | ٠    | 82    | 4  |
| Drosophila melanog | ABB66457 | 22 | 555   | •    | 82    | చ  |
| Bacillus subtilis  | AAW98149 | 20 | 2285  | 7.4  | 83    | ະ  |
| Histamine binding  | AAY18083 | 20 | 207   | 7.4  | 83    | ï  |
| I. scapularis Salp | AAY97773 | 22 | 217   | 7.5  | 84    | ŏ  |
| Listeria monocytog | ABB48437 | 23 | 917   |      | 84.5  | 89 |
|                    | AAG17989 | 21 | 441   |      | 85    | 8  |
|                    | AAG17990 | 21 | 437   |      | 85    | 27 |
|                    | ABG03896 | 22 | · 411 |      | 85    | 8  |
| Arabidopsis thalia | AAG17991 | 21 | 254   |      | 85    | 8  |
| Drosophila melanog | ABB58683 | 22 | 2778  | 7.6  | 86    | 24 |
| quence of          | AAR37467 | 14 | 202   |      | 91    | ü  |
| I. scapularis Salp | AAY97764 | 22 | 221   | 8.7  | 97.5  | ະ  |
| cus 1              | AAU35203 | 22 | 722   |      | 102.5 | 2  |
| Histamine binding  | AAY18089 | 20 | 321   |      | 126.5 | õ  |
|                    | AAY18087 | 20 | 285   | 11.3 | 127.5 | 6  |
| Histamine binding  | AAY18088 | 20 | 284   |      | 140   | 8  |
|                    | AAB73260 | 22 | 172   | 21.2 | 239   | 7  |
|                    | AAB74288 | 22 | 172   |      | 239   | 9  |
| Histacalin protein | AAB73262 | 22 | 182   |      | 251.5 | 5  |
| Histacalin protein | AAB74290 | 22 | 182   |      | 251.5 | 4  |
| tamine             | AAY18078 | 20 | 190   |      | 252   | ω  |
| k vasoa            | 374      | 19 | 190   |      | 252   | ีผ |
| ď                  | AAY18080 | 20 | 200   | 23.6 | 265   | F  |
| Tick vasoactive am | AAW37448 | 19 | 200   |      | 265   | 5  |
|                    |          |    |       |      |       |    |

# ALIGNMENTS

| 7 1<br>449<br>AAW37449 standard; Protein; 209 AA.<br>AAW37449; |
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| ,<br>,   |

Vasoactive amine binding protein; D.RET6; histamine; serotonin; assay; antihistamine; anti-inflammatory; insect bite; snake bite; scorpion bite; dermatitis; vaccine; transgenic animal; tick.

| PΙΧ                | PA X                | PR              | PR<br>R       | Y P             | X | PD           | × | PN            | × | FΤ                  | ΕŢ   | FH                  | × | လ                        | XX | KW                          | KΨ   | KW                          | × |
|--------------------|---------------------|-----------------|---------------|-----------------|---|--------------|---|---------------|---|---------------------|------|---------------------|---|--------------------------|----|-----------------------------|--|-----------------------------|---|
| Nuttall PA, Paesen | (OXFO-) OXFORD VACS | 18-MAY-1996; 96 |               | 19-MAY-1997; 97 |   | 27-NOV-1997. |   | WO9744451-A2. |   |                     | tide | Key L               |   | Dermacenter reticularis. |    | scorpion bite; dermatitis;  | assay; antihistam                            | Vasoactive amine            |   |
| en GC;             | CS LTD.             | 96GB-0010484.   | 97GB-0007844. | 97WO-GB01372.   |   |              |   |               |   | /label= Sig_peptide | 128  | Location/Qualifiers |   | ularis.                  |    | rmatitis; vaccine; transgen | assay; antihistamine; anti-inflammatory; ins | binding protein; D.RET6; hi |   |

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC This protein comprises tick Dermacenter reticularis (Dr) novel CC vascactive amine binding protein (VABP) D.RET6. Its amine acid CC sequence was deduced from a CDNA clone (see AANO0230) obtained CC from a Dr salivary gland cDNA library. 3 Novel VASPs, designated CC FS-HBP1, FS-HBP2 and MS-HBP1 (see AAN3746-48), of the tick Rhipicephalus appendiculatus have also been identified. The CC vABPs can be expressed in host cells using e.g. a baculovirus of the vascast of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.
                                                                                                                                                                    Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allerging asthma; urticaria; urticaria; allerging asthma; urticaria; urticar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vasoactive amine binding proteins and related nucleic vectors - transformed cells and transgenic animals, used assaying or removing histamine and as antihistamine or
   Rhipicephalus
                                                                                                                                                                                                                                                                                                                                 Histamine
                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY18081 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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llarity 100.0%;
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Pred. No. 3.9e-104;
0; Mismatches 0;
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RESULT 3
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AC AAY1
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DT 06-P
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DE Hist
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KW Hist
KW Gasth
KW asth
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                                                                                                                                      AAY18086 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histamine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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26-NOV-1997;
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209; Conser
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                                                                                                                                                                                                                                                       GYKNIRNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNADQGCELWVKKSHYKHVPDYCT
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llarity 100.0%;
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97GB-0025046.
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                                                                                                                                         Protein;
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Pred. No. 3.9e-104;
; Mismatches 0;
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val of histamine
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120 180

60

Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhintits; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine

Histamine binding 06-AUG-1999

protein

Ih/Bm-HBP2

(first entry

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RESULT 4
AAY18085
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AC AAY1
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Best Local S
Matches 75
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  06-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histamine and serotonin binding compounds useful for the treatment of allergies % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                              AAY18085
                                                       AAY18085 standard;
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26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-357841/30.
                                                                                                                              183
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75; Conserv
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                                                                                                                                           FCAKDRKTYDIFNEECV 202
                                                                                                                            -VALGRITYNISTPNCV 198
                                                                                                                                                                                  KNIIQWTTENNTKFNDTVVFTDGQTCDVLYIPYKEDGYELWVRSEYLQNTPTCCQFIFDL
                                                                                                                                                                                                   RNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNADQGCELWVKKSHYKHVPDYCTFVFNV
                                                                                                                                                                                                                                         NDS-VWGKNFTCLSVTVTSKYESTFTVEYNTTYKNQSQ--QWVSMSENVTAVQEGGY-SV
                                                                                                                                                                                                                                                                   NDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYYNVTETVKAVFQYGYKNI
                                                                                                                                                                                                                                                                                               VLLLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYE
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  (first entry)
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97GB-0025046.
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                                                         Protein;
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                                                                                                                                                                                                                                                                                                                                                                  32.4%; Score 364; DB 2
38.1%; Pred. No. 4e-28;
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                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Histamine and serotonin binding compounds useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX76970.
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26-NOV-1997;
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176 CQFIFDL-VALGRTTYNISTPDCV
                                                                                                                                         60 FLRSTYNNDS-VWGKNETCLSVTVTSKHESTETVEVNTTYKNQSQ--QWVSMTENVTAVQ
                                                                                                                                                                                                                                                  1 MKMQVVLLLTFVSAALATQAETTSAKAG--ENPLWAHEELLGKYQDAWKSIDQGVSVTYV
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                          QYGYKNIRNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNADQGCELWVKKSHYKHVPDY 178
                                                                                                                                                                           LAKTTYENDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYYNVTETVKAVF 118
                                                                                                                                                                                                                  MKALLIAVGYLAAVTAAPQASPSSPRNEPLKNTTW-HSKELKNYQDAWKSINQNVSTTYY 59
                                 CTFVFNVFCAKDRKTYDIFNEECV
                                                                     EEGY-DVKNIIQWTTENNTKFNDTVVFTDGQTCDLLYIPYKENGYELWVRSDYLQNTPTC
                                                                                                                                                                                                                                                                                                                                                               203
                                                                                                                                                                                                                                                                                        Conservative
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97GB-0025046.
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                                                                                                                                                                                                                                                                                                       31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                      Score 353; DB 20;
Pred. No. 5.1e-27;
1; Mismatches 81;
 198
                                 202
                                                                                                                                                                                                                                                                                        81;
                                                                                                                                                                                                                                                                                                                          Length
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RESULT 5
AAW37447
                                                                        from a salivary gland cDNA library. FS-HSP1 (see AAW37446) and male-specific HSP1 (see AAW37446) and a related protein, D.RET6 (see CAW37449) from Dermacenter reticularis, were also identified. These convel vasoactive amine binding proteins (VABPs) can be expressed in host cells using e.g. a baculovirus expression system. They can be used: (i) to assay histamine (or other VA such as serotonin) in body fluids or cell culture supernatants, e.g. to monitor the effect of allergens; (ii) for binding VA, e.g. to remove histamine or anti-inflammatory agents, e.g. for treating insect, snake or scorpion bites or dermatitis, or as a carrier for slow release of histamine-related compounds; (iv) in vaccines to protect against metazoan parasites, especially in animals; (v) as reagents for the studying inflammation, involvement of VA in ulcer formation or the
                                                                                                                                                                                                                                                                                                                                                                                                                      New vasoactive amine binding proteins and related nucleic vectors - transformed cells and transgenic animals, used f assaying or removing histamine and as antihistamine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1997
                                                                                                                                                                                                                                                                                                                        female-specific
                                                                                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                     anti-inflammatory agents
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18-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhipicephalus appendiculatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          histamine; serotonin; assay; antihistamine; anti-ininsect bite; snake bite; scorpion bite; dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Female-specific vasoactive amine binding protein 1; FS-HCP1; histamine; serotonin; assay; antihistamine; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tick vasoactive amine binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW37447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW37447 standard; Protein;
                                                                                                                                                                                                                                                                     protein comprises tick Rhipicephalus appendiculatus (Ra) novel le-specific histamine binding protein 2 (FS-HBP2). Its amino sequence was deduced from a cDNA clone (see AAW00228) obtained a salivary gland cDNA library. FS-HSP1 (see AAW37446) and september specific HSP1 (see AAW37448) and a related protein, D.RET6 (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-018506/02
                                        ng inflammation, involvement of VA in ulcer formation or response etc. VABPs provide a more sensitive assay for the than low-affinity antibodies currently used. They me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA,
                                more
                                                                                                                                                                                                                                                                                                                                                                       2; Fig 2; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OXFORD
190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              animal; tick.
                                effective
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96GB-0010484.
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                            than
                              conventional
                              antihistamines
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LLLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKTTYEN

Query Match Best Local : Matches

72; Conser

Conservative

32;

Score 290.5; DB 19; Pred. No. 8.1e-21; 2; Mismatches 79;

Indels

Gaps

66 9

Best Local Similarity

25.8%; 36.0%;

Score Pred.

290.5; DB 2 No. 8.1e-21;

20;

Length 190

Query Match

Sequence

190

B

Length

190; 17;

25.8%;

Sequence

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RESULT 6
AAY18079
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                                     This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking
                                                                                                                                                                                                                                                                                             Histamine and serotonin binding of allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.
                                                                                                                                                                                                                                                            Claim 1; Fig
                              ectoparasites
                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-357841/30
                                                                                                                                                                                                                                                                                                                                                                                               Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Histamine binding protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY18079 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                             (OXFO-) OXFORD VACS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1998;
26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhipicephalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Histamine binding protein FS-HBP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNEY-AVGRETRDVFTSACL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNAD---QGCELWVKKSHYKHVPDYCTFV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNVFCAKDRKTYDIFNEECV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENAFRYETEDGQVFTDVIAYSD-DNCDVIYVPGTDGNEEGYELWT--TDYDNIPANCLNK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DP-VWGNDETCVGVMANDVNEDEKSIQAEFLFMNNADTNMQF--ATEKVTAVKMYGY-NR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTGSWGSQFKCLQVQEIERKEEDYTVTSVFTF-RNASSPIKYYNVTETVKAVFQYGYKNI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLILSLALVLA-----LSQVKGNQPDWADEAANGAHQDAWKSLKADVENVYYMVKATYKN 57
                                                                                                                                                                                                                                                              2; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             appendiculatus
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97GB-0025046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serotonin binding compound;
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                                                                                                                                                                                                                                                                                                            compounds useful
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RESULT 7
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                                            This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used as components of vaccines directed against blood-sucking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 6; 84pp; English
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N-PSDB; AAX76969.
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26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Histamine and serotonin binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergies
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|| : | |:| |:| |:
FNEY-AVGRETRDVFTSACL 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNAD----QGCELWVKKSHYKHVPDYCTFV
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97GB-0025046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compounds useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₿
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of histacalin proteins for treating or preventing conjunctivitis, or for manufacturing a medicament for preventing conjunctivitis, e.g. seasonal or perennial
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                                                                                                                                                                                                                                                                                                                    is the histacalin point the treatment of
                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the use of a histacalin protein
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                                                                                                                                                                                                                                                                                                               treating or preventing conjunctivitis. The present sequence the histacalin protein FS-HBP1. The invention is particularly the treatment of allergic or seasonal conjunctivitis.
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     08-JUN-1998
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                                                      AAW37448;
                                                                                                 AAW37448 standard; Protein;
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29; Mismatches
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                                                                                                                                                                                                                        This protein comprises tick Rhipicephalus appendiculatus (Ra) novel CC male-specific histamine binding protein (MS-HBP1). Its amino CC acid sequence was deduced from a cDNA clone (see AAV0027) obtained CC from a salivary gland cDNA library. Female-specific HSP1 and CC HSP2 (see AAW37446-47) and a related protein, D.RET6 (see AAW37449) CC from Dermacenter reticularis, were also identified. These novel CC bost cells using e.g. a baculovirus expression system. They can be used: (i) to assay histamine (or other VA such as serotonin) in CC bedy fluids or cell culture supernatants, e.g. to monitor the ceffect of allergens; (ii) for binding VA, e.g. to remove histamine or cc from blood, food, cell cultures etc.; (iii) as an antihistamine or cc anti-inflammatory agents, e.g. for treating insect, snake or scorpion bites or dermatitis, or as a carrier for slow release of histamine-related compounds; (iv) in vaccines to protect against commune response etc. VABPs provide a more sensitive assay for histamine than low-affinity antibodies currently used. They may compared the componed of the component of VA in ulcer formation or the listamine than low-affinity antibodies currently used. They may compared the component of the
                                                                                            Matches
                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New vasoactive amine binding proteins and related nucleic acid, vectors - transformed cells and transgenic animals, used for assaying or removing histamine and as antihistamine or anti-inflammatory agents
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 3; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV00229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OXFO-) OXFORD VACS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-1997;
18-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09744451-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhipicephalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insect bite; snake bite; scorpion bite; dermatitis; vaccine;
transgenic animal; tick.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              histamine; serotonin; assay; antihistamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Male-specific vasoactive amine binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tick vasoactive amine binding protein 1 MS-HBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998-018506/02.
                                               w
                                                                                               69;
                          MQVVLLLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKT
  MKVLLLV--LGAALCQNADA-----NPTWANEAKLGSYQDAWKSLQQDQNKRYYLAQA
                                                                                                                                                                                    200 AA;
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paesen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    appendiculatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97GB-0007844
96GB-0010484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-GB01372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Sig_peptide 79..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Asn is N-glycosylated"
                                                                                                                  23.6%;
                                                                                            34;
                                                                                          Score 265; DB 19;
Pred. No. 3.1e-18;
4; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein 1; MS-HCP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-inflammatory;
                                                                                                                                       Length
                                                                                            Indels
                                                                                            26;
                                                                                            Gaps
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TYENDIGSWGSQFKCLQV--QEIERKEEDYTVISVFTFRNAS-SPIKYYNVTETVKAVFQ

TQTTD-GVWGEEFTCVSVTAEKIGKKKLNATI----LYKNKHLTDLKESHETITVWKAYD

106

62 51

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AAY180
AAY180
AAY180
AAY180
AAY AAY180
AC AAY1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                       Matches
                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                       This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used as components of vaccines directed against blood-sucking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Histamine and serotonin binding compounds useful of allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-357841/30
N-PSDB; AAX76966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY18080 standard; Protein; 200 AA.
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 3; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuttall PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-1998;
26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9927104-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhipicephalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Histamine binding protein MS-HBP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY18080
                                                                                                                                                                                                                                                                                                        ectoparasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OXFO-) OXFORD VACS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 KIPDCCKFTMAYFAQQQEKT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                       69; Conser
                            MQVVLLLTFVSAALATQAETTSAKAGENPLMAHEELLGKYQDAWKSIDQGVSVTYVLAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVPDYCTFVFNVFCAKDRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGYKNIRNAIEYQVGGGLNIT--DTLIFTDGELCDVFYVP---NADQG-CELWVKKSHYK
MKVLLLV - - LGAALCQNADA - - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y---TTENGIKYETQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSDEGDYELWVSEDKID 163
                                                                                                                                                                                                                                            200
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paesen GC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           appendiculatus.
                                                                                                                                                                                                                                            ₹
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97GB-0025046.
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                                                                                                                                          23.6%;
                                                                                                                 Score 265; DB 20;
Pred. No. 3.1e-18;
4; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193
-NPTWANEAKLGSYQDAWKSLQQDQNKRYYLAQA
                                                                                                                                                                          Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for the treatment
                                                                                                                    26;
                                                                                                                 Gaps
51
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RESULT 12
AAW37446
ID AAW377
XX AAW377
XX O8-JU
DT 08-JU
DE T1Ck
XX Femal
KW Hista
KW Hista
KW Hista
KW Hista
KW Hista
KW Hista
XX Femal
KW Hista
XX Femal
XX Femal
XX Femal
XX Femal
XX Inge
FT Pepti
XX W097
PN W097
PN W097
PN W097
PN W097
PN Nutt
XX Inge
PT 18-A
PR 18-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New vasoactive amine binding proteins and related nucleic ac vectors - transformed cells and transgenic animals, used for assaying or removing histamine and as antihistamine or anti-inflammatory agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Female-specific vasoactive amine binding protein 1; FS-HCP1; histamine; serotonin; assay; antihistamine; anti-inflammatory; insect bite; snake bite; scorpion bite; dermatitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tick vasoactive amine binding protein 1 FS-HBP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuttall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-1997;
18-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhipicephalus appendiculatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transgenic animal; tick.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW37446 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 1; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9744451-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OXFO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-018506/02.
DB; AAV00227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 TYENDTGSWGSQFKCLQV--QEIERKEEDYTYTSVFTFRNAS-SPIKYYNVTETVKAVFQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OXFORD VACS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVPDYCTFVFNVFCAKDRKT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIPDCCKETMAYFAQQQEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y---TTENGIKYETQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSDEGDYELWVSEDKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGYKNIRNAIEYQVGGGLNIT--DTLIFTDGELCDVFYVP---NADQG-CELWVKKSHYK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQTTD-GVWGEEFTCVSVTAEKIGKKKLNATI----LYKNKHLTDLKESHETITVWKAYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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96GB-0010484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183
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This protein comprises tick Rhipicephalus appendiculatus (Ra) novel female-specific histamine binding protein 1 (FS-HBP1). Its amino acid sequence was deduced from a cDNA clone (see AAV0227) obtained from a salivary gland cDNA library. FS-HSP2 and male-specific thispalling from a salivary gland cDNA library. FS-HSP2 and male-specific thispalling from a salivary gland cDNA library. FS-HSP2 and male-specific thispalling from between the first protein, D.RETG (see AAW37449) and a related protein, D.RETG (see AAW37449) from Dermacenter reticularis, were also identified. These novel vasoactive amine binding proteins (VABPs) can be expressed in host cells using e.g. a baculovirus expression system. They can be used: (i) to assay histamine (or other VA such as serotonin) in body fluids or cell culture supernatants, e.g. to monitor the effect of allergens; (ii) for binding VA, e.g. to remove histamine or anti-inflammatory agents, e.g. for treating insect, snake or canti-inflammatory agents, e.g. for treating insect, snake or securious proteins of the complex proteins of the com

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RESULT 13
AAX18078
ID AAX18
XX AAX18
AC AAX18
AC
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Best Local S
Matches 68
This sequence is an example of a histamine or serotonin binding compound (\lambda), of the invention. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug and lergy; abnormary coronary disease; coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma: urticaria; allergic rhinitis; atopic demantitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator;
                                                                                                                                   Claim 1; Fig 1; 84pp;
                                                                                                                                                                                                                                                                                                                                                 Nuttall
                                                                                                                                                                                                                                                                                                                                                                                                 (OXFO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-1998;
26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhipicephalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histamine binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY18078 standard; Protein; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 studying
                                                                                                                                                                                      allergies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                                                                                              PA,
                                                                                                                                                                                                                                                                                                                                                                                                 OXFORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEKFNEYAA-GLPVRDVYTSDCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYENDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYYNVTETVKAVFQYGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - NKENAITYQTEDGQVLTDVLAFSD-DNCYVIYALGPDGSGAGYELWA--TDYTDVPASC
                                                                                                                                                                                                              and serotonin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190
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                                                                                                                                                                                                                                                                                                                                              Paesen
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97GB-0025046
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Pred. No. 5.7e
28; Mismatches
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.7e-17;
                                                                                                                                                                                                                useful
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                                                                                                                                                                                                              for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 190;
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RESULT 14
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Best Local :
                                                                                                      Use of histacalin proteins for treating or preventing conjunctivitis, or for manufacturing a medicament for preventing conjunctivitis, e.g. seasonal or perennial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and druallergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking
                                                                     Claim 4;
                                                                                            conjunctivitis
                                                                                                                                                                              Nuttall PA,
                                                                                                                                                                                                                              01-SEP-1999;
                                                                                                                                                                                                                                                      24-AUG-2000;
                                                                                                                                                                                                                                                                             08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                  Histacalin;
                                                                                                                                                                                                                                                                                                                                                                       Histacalin protein MS-HBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB74290
                                                                                                                                                                                                      (EVOL-) EVOLUTEC LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         humans) and in
                                                                                                                                                        2001-257675/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 TYKNDP-VWGNDETCVGTAAQNLNEDEKNVEAWFMFMNNADTV-YQHTFEKATPDKMYGY 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFVFNVFCAKDRKTYDIFNEECV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NKENAITYQTEDGQVLTDVLAFSD-DNCYVIYALGPDGSGAGYELWA--TDYTDVPASC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNIRNAIEYQVGGGLNITDTLIFTDGELCDVFYVPNAD----QGCELWVKKSHYKHVPDYC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYENDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYYNVTETVKAVFQYGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOVVLLLTFVSAALATQAETTSAKAGENPLWAHEELLGKYQDAWKSIDQGVSVTYVLAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEKFNEYAA-GLPVRDVYTSDCL
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nilarity 33.5%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                  MS-HBP1;
                                                                                                                                                                              Paesen
                                                                                                                                                                                                                                                      2000WO-GB03282
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                     5-6;
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                                                                                                                                                                                                                              99GB-0020674
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                                                                    19pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                              GC;
                                                                                                                                                                                                                                                                                                                                                  conjunctivitis.
                                                                    English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 252; DB
Pred. No. 5.7e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20;
.7e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 190;
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                                                                                                       non-infective
c treating or
l allergic
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The present invention relates to the use of a histacalin protein for treating or preventing conjunctivitis. The present sequence is the histacalin protein FS-HBPI. The invention is particularly in the treatment of allergic or seasonal conjunctivitis.

protein

useful

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Sequence

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ARESULT 15
AAB73262
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Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for treating or preventing allergic rhinitis. The method involves employing a blood-feeding ectoparasite-derived (e.g. tick-derived) instructain protein. The present sequence is one such histacalin protein. The histacalin protein, is useful for treating or preventing allergic rhinitis, both seasonal and perennial allergic conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of histacalin proteins for treating or preventing allergic rhinitis, or for manufacturing a medicament for treating or preventing allergic rhinitis, e.g. seasonal or perennial allergic rhinitis
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Pages 4-6; 19pp; English.
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EDYTYTSVFTFRNAS-SPIKKYNVTETVKAVFQYGYKNIRNAIEYQVGGGLNIT--DTLI 144 : | : | : | : | : | : | : | : | : |
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Search completed: August 4, 2003, 17:14:39
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1: sp_archea:*
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6: sp_mammal:*
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| Q8y763 listeria mo | Q05508 trypanosoma | Q97ay2 thermoplasm |              | 006915 lactobacill | Q95ly3 macaca fasc | Q9gp33 echinococcu | Q93214 staphylococ | Q8pqg5 xanthomonas | Q8rin4 fusobacter1 | Q8r7c5 thermoanaer | Q8x116 clostridium | Q8e147 shewanella | Q8dyv2 streptococc | Q8e4g0 streptococc | 096170 plasmodium | Q8f3f9 leptospira | O31951 bacillus su | 064070 bacteriopha | P87514 border dise | Q8ils3 plasmodium | Q90193 agaricus bi |               | Q81jw5 plasmodium | Q43079 pisum sativ | Q8yanl listeria mo | 061096 trypanosoma | Q816a8 theobroma c |  |

# ALIGNMENTS

RESULT 1 Q8WSK7

| Qy 60 LNATILYKNKHL/  | Query Match 25.4%; Some Best Local Similarity 35.3%; Pure Conservative 29; Matches 61; Conservative 29; Oy 1 NPTWANEAKLGSYQDAWKSIQO  | OS Dermacentor reticulatus.  OE Eukaryota; Metazoa; Arthropoda; Chelicerata; Al OC Parasitiformes; Ixodida; Ixodidae; Dermacentor. OX NCBI_TaxID=57047; RN [1] RN SEQUENCE FROM N.A. RA Sangamnadech S., Paesen G.C., Nuttall P.A.; RT "A high affinity serotonin- and histamine-bindi RT by blood-feeding ticks."; RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ of REMBL; AF217101; AAL56644.1; - DR EMBL; AF217101; AAL56644.1; - DR InterPro; IPR002970; His_binding. DR Pfam; PF02098; His_binding; 1 SEQUENCE 209 AA; 23889 MW; E5EB8BE710859591 | Q8WSK7 Q8WSK7; QBWSK7; O1-MAR-2002 (TrEMBLrel. O1-MAR-2002 (TrEMBLrel. O1-JUN-2002 (TrEMBLrel. O1-JUN-2002 (TrEMBLREN. |
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| LNATILYKNKHLTDLKESHETITVWKAYDYTENGIKYETQGTRTQTFEDVFV 112 : :  :    : | 25.4%; Score 251.5; DB 5; Length 209; similarity 35.3%; Pred. No. 2.1e-14; Conservative 29; Mismatches 66; Indels 17; Gaps 8;  NPTWANEAKLGSYODAWKSLQQDQNKRYYLAQATQTTD-GVWGEEFTCVSVTAEKIGKKK 59       : | Dermacentor reticulatus.  Dermacentor reticulatus.  Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acarl;  Eukaryota; Metazoa; Ixodida; Ixodidae; Dermacentor.  ENGLI_TaxID=57047;  [1]  [1]  [1]  [2]  [3]  [3]  [3]  [3]  [4]  [5]  [5]  [5]  [5]  [6]  [6]  [6]  [6   | ; PRT; 209 AA.  20, Created)  20, Last sequence update)  21, Last annotation update) binding protein.                  |

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01-NOV-1996 (TREMBLRel. 0
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Johnston M., Andrews S., Brinkman R., Cooper J., Lary Johnston M., Fulton L., Gattung S., Greco T., Kirsten J Hallsworth K., Hawkins J., Hiller L., Jier M., Johnso Johnston L., Langston Y., Latrelle P., Le T., Mardis Johnston L., Langston Y., Latrelle P., Le T., Mardis Johnston L., Langston Y., Peluso D., Rifken L., I
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Q05583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00320; WD40; 7.

PROSITE; PS00678; WD_REPEATS_1; 1.

PROSITE; PS50082; WD_REPEATS_2; 5.

PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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Taich A., Trevaskis E., Vignati D., Wilcox L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C;
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                    VPKERGSDEGDYELWVSE
                                                                                                                                                                                                                                     KHLTDLKESHETITVWKAYDYTTE-----NGIKYETQGTRTQTFEDVFVFSDYKNCDVIF
                                                                                                                                                                                                                                                                                   AW-----SNDGYYLATCSR-DKSVWIWETDESGEEYECISVLQEH--SQDVKHVIWHPS
                                                                                                                                                                                                                                                                                                                           AWKSLQQDQNKRYYLAQATQTTDGVW------GEEFTCVSVTAEKIGKKKLNATILYKN
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                                                                                                               VWKYMGDDEDDQQEWVCE
                                                                                                                                                                                               EALLASSSYDDTVRIWKDYDDDWECVAVLNGHEGTVWSSDFDKTEGVFRLCSGSDDSTVR
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      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
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27.5%;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 113.5;
Pred. No. 0.0
      PRT.;
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Best Local
                                                                                                                                                                                                                                                                                                                             STÄRIN-Rhode Island; TISSUE-Salivary gland
Valenzuela J.G., Francischetti I.M., Pham
Mather T.N., Ribeiro J.M.C.;
"Exploring the Sialome of the Tick Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative 22.5 kDa secreted protein.
Ixodes scapularis (Black-Legged tick) (Deer tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Parasitiformes; Ixodida; Ixodidae; Ixodes.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative secreted histamine binding protein.
Ixodes scapularis (Black-Legged tick) (Deer tick)
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arac
Parasitiformes; Ixodida; Ixodidae; Ixodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Rhode Island; TISSUE=Sallvary gland; Valenzuela J.G., Francischetti I.M., Pham V.M., Garfield M Mather T.N., Ribeiro J.M.C.; "Exploring the Slalome of the Tick Vector of Lyme Disease, scapularis.";
                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-Rhode Islan
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                                                                                                                                                                                                                                                                EMBL; AF483742;
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                                                                                                                                                                                                                                                                                                               scapularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6945;
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                                                                                                                                                                Similarity
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                                              DEKYWQYQDIQRALNNPDRESWLYYRTYRRETD-
                                                                                        EAKLGSYQDAWKSLQQ-DQNKRYYLAQATQTTDGVWGEEFTCVS----
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                                                                                                                                                                                                                                                                (FEB-2002) to the EMBL/GenBank/DDBJ databases 3742; AAM93664.1; -.
                                                                                                                                                                                                                                       210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 AA;
                                                                                                                                            Conservative
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                                                                                                                                                                                                                                          24689 MW;
                                                                                                                                                           9.78;
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                                                                                                                                       Score 95.5; DB
Pred. No. 1.1;
30; Mismatches
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5; Mismatches
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Pred. No. 0.
                                                                                                                                                                                                                                       C5B75614649A9BED CRC64;
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                                                                                                                                                                                                                                                                                                                                                                            gland;
Pham V
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                                                                                                                                                                                                                                                                                                                                  Lyme
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Best Local S
Matches 47
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative secreted histamine binding protein.
Ixodes scapularis (Black-legged tick) (Deer tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachni
Parasitiformes; Ixodida; Ixodidae; Ixodes.
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative secreted protein.
Ixodes scapularis (Black-legged tick) (Deer tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Ixodes.
                                                                                                                 STRAIN-Rhode Island; TISSUE-Salivary Valenzuela J.G., Francischetti I.M., Valenzuela J.G., Ribeiro J.M.C.;
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                                           Submitted
                                                               scapularis.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                       "Exploring the Sialome of the Tick Vector of Lyme
                                                                                                                                                                                                                                                            NCBI_TaxID=6945;
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           tted (FEB-2002) to the AF483717; AAM93639.1;
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                                     EMBL/GenBank/DDBJ databases
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RA Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A.,
RA Ishii S., Yamashoto J., Isono Y., Kawai-Hio Y., Sato H., Wakamatsu A.,
RA Kihura K., Yamashita H., Matsuo K., Nakamura Y., Sakine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO93308; BACO4128.1; -.
SR EMBL; AKO93308; BACO4128.1; -.
SEQUENCE 581 AA; 66121 MW; 979A8B4DE2177C74 CRC64;
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Best Local :
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation updat
Hypothetical protein FLJ35989.
Homo sapiens (Human).
Q81BIO PRELIMINARY;
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Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                  N-PVVMVDREKKRLVELLKDLDEKDSGLSSSEGDQSGWV
                                                                                                                                                                                                                                                      NCDVIEVPKER--
                                                                                                                                                                                                                                                                                                                EMQMQKLNKDFTCDVERNESLIKSGKKPFSNTE---KIELRGKHNQDFIKRNIELAKESR
                                                                                                                                                                                                                                                                                                                                                                 NATILYKNKHLT-DLKESHETITVWKAYDYTTENGIKYETQGTRTQTF--EDVFVFSDYK
                                                                                                                                                                                                                                                                                                                                                                                                                        W-EEIKSAKYSEAWQSKEEMENTKKFLSLTAVSEETVGPSHEEEDTFSSVFHTQIPPEEY
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 92;
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                                                            PRT;
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Q92BX7;
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005273;
01-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oudega B., Koningstein G., Duesterhoeft A.;
"Bacillus subtills genome project, DNA sequence from yucA to submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z93940; CAB07966.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
SEQUENCE 1
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Quail M., Barrell B.;
Submitted (SEP-2002) to the
EMBL; AL844506; CAD51020.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical YUCC.
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01-MAR-2003
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                                                                                                                                        145
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33; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 AA; 1
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(TrEMBLrel.
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(TIEMBLrel. 04, Last sequence up
(TIEMBLrel. 19, Last annotation
19.8 kDa protein.
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26.9%;
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  19,
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exa; Haemosporida;
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Pfam; PF02518; HATPASe_C; 1.
Pfam; PF00512; HiskA; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00304; HAMP; 1.
SMART; SM00387; HAMP; 1.
SMART; SM00388; HISKA; 1.
                                                                                                                                                        01-MAY-2000
01-MAY-2000
01-MAR-2003
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                                                               Listeria monocytogenes
Bacteria; Firmicutes; I
                                                                                                          LISK (Two-component sensor LISK OR LMO1378.
                                                                                                                                                                                                                                                         Q9RPY9
SEQUENCE
                                    NCBI_TaxID=1639;
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EMBL; AL596168; CAC96646.1; -.
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InterPro; IPR005467;
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Bacteria; Firmicutes;
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Pred. No. 18;
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
A Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
A Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Lentian K.-D., Fsihl H., Garcia-del Portillo F., Garrido P.,
A Lentian K.-D., Fsihl H., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
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A Madueno E., Maitournam A., Mata Vicente J., Nedjari H.,
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A Madueno E., Maitournam A., Mata Vicente J., Nedjari H.,
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A Madueno E., Maitournam A., Mata Vicente J., Nedjari H.,
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Best Local 9
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InterPro; IPR003467; His_kinase.
Pfam; PF00672; HAMP; 1.
Pfam; PF002518; HATPASe_C; 1.
Pfam; PF00512; HiSKA; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00304; HAMP; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00388; HiSKA; 1.
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08K3S1;

01-OCT-2002 (TrEMBLrel. 2

01-OCT-2002 (TrEMBLrel. 2

01-MAR-2003 (TrEMBLrel. 2
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"Identification and disruption of lists, a genetic
two-component signal transduction system involved
and virulence in listeria monocytogenes.";
J. Bacteriol. 181:6840-6843(1999).
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EMBL; AL591978; CAC99456.1; -.
ListLiList; LM001378; -.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR003660; HAMP.
Mus musculus (Mouse).
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Kinase; Phosphorylation; Sensory transduction; Transferase;
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MEDLINE-21537279; PubMed-11679669;
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MEDLINE-20011355; PubMed-10542190;
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RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamiln N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Cliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
RA Gliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Ra Regger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G;
"Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).

EMBL; ALO34557: CAD49096.1; -.

SQ SEQUENCE 3467 AA; 398212 MW; E8FCBA37025989D2 CRC64;
  Query Match
Best Local S
Matches 46
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Best Local
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Jones L., Eggen A., Avner P., Duret L.;
"Comparative sequence analysis of the X-
mouse, human and bovine.";
Genome Res. 12:894-908(2002).
EMBL; AJ421480; CAD33962.1; -
InterPro; IPR001254; Ser_protease_Try.
SMART; SM00020; Tryp_SPC; 1.
PROSTTE; PS50240; TRYPSIN_DOM; 1.
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Mammalia; Eutheria; |
NCBI_TaxID=10090;
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Q81218;
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Eukaryota; Alveolata; Apicomplexa; H
NCBI_TaxID=36329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNPAVIIRTAPYET ---WIKQFI-----KVSKKLLNPTRSLHCRTLYENEYVPQIRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protease; Serine pr
604 AA; 67709 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TremBLrel. 23, Created)
(TremBLrel. 23, Last sequence update)
(TremBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed-12368867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.7%;
                             8.7%;
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Score 86.5; D
Pred. No. 2.1e
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5542092EBFEA8ACD CRC64;
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DB 5;
2.1e+02;
nes 63;
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RESULT 15
Q8F3F8
ID Q8F3F
AC Q8F3F
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
CON LA24
GN LA24
GN LA24
GN LA24
GN LA21
RN [1]
RN [1]
RP STRAI
RA Ren S
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Q8FQ6

ID Q8FQ6

AC Q8FQ6

AC Q8FQ6

DT 01-MA

DT 01-MA

DT 01-MA

DT 01-MA

CONSE

GN CED126

OS COTYT

OC Bacte

OC COTYT

ON NCBT

RN [1]

RN [1]

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RA Kawall

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DR EMBL;

KW Hypot
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Best Local S
Matches 40
                                                                                                                                               Q8F3F8;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,

Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,

Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

Usuda Y., Sugimoto S.;

"The entire genomic sequence of Corynebacterium efficiens YS-314.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AP005218; BAC18075.1; -.

Hypothetical protein; Complete proteome.

BEQUENCE 391 AA; 42871 MW; 07C46C6DE4F411F0 CRC64;
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                            Leptospira interrogans.
Bacteria; Spirochaetes;
Bact_TaxID=173;
                                                                                                                                                                                                                        Q8F3F8
            STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
                                 SEQUENCE FROM N.A.
                                                                                                                      LA2448
                                                                                                                                    Putative outermembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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                                                                                                                                                                                                                                                                                                                                NCDVIFVPKERGSD----EGDYEL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                               RVWFSGAPETTDFHDLDPTRVGGEVNSGNVLVVTASKGHAEVEQVPVGKWVFEAL----N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYYLAQATQTTD-----GVWGE--EFTCVSVTAEK-----IGKKKLNATILYKN 68
                                                                                                                                                                                                                                                                                                            ---ASLKPRERTTDLVLEPGDEEL 348
                                                                                                                                                                                                                                                                                                                                                                                                              KHLTDLKESHETITVWKAYDYTTENGIKYETQGTRT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKTVRN------VYTDS-----SCKPAP 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FCREREKKEEVVEKKCKKDHEGCNKPNT--KGNHGCVSACKDYEEYISTKKKQYNTQ---
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                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.7%; Score 86; DB
27.8%; Pred. No. 17;
Live 15; Mismatches
                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
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23, Last sequence update)
23, Last annotation update)
                                                                                  Spirochaetales;
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                                                                                                                                                                                                                        PRT;
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                                                                              Leptospiraceae;
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Best Local 9
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138
                           103
                                                      78
                                                                                65
                                                                                                           29
                                                                                                                                                                 38;
                                                                                                                          Similarity
                                                LFDNRLKTLPKEIGQLKNIQELNLSSNQLTILPKEIGKLENLQRLDLYDNRLTILPIEIG 137
KLQNLQTLYLSSN----QLTTLPRESGKLENLQELNLSDNQLTTLP
                         RTOTFEDVFVFSDYKNCDVIFVPKERGSDEGDYELWVSEDKIDKIP
                                                                                LYKN-----KHLTDLKESHETITVWKAYDYTTENGIK---YETQGT-----
                                                                                                          ADEVKPGTYMDLTKALQNPLNVRVL-----DLSGQNFTTLPKEIEQL--KNLQKLY
                                                                                                                                                                 Conservative
                                                                                                                                                              8.6%; Score 85.5; I
22.9%; Pred. No. 21;
tive 31; Mismatches
                                                                                                                                                                                           DB 16;
                                                                                                                                                                 60;
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                                                                                                                                                                 Indels
                         148
                                                                                                                                                                                            428;
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Search completed: August Job time: 54.3467 secs 2003, 12:20:01

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Minimum
Maximum
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No.
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Perfect score:
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11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB DB
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989
1 NPTWANEAKLGSY
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RB4A_ECHMI
OPPF_MYCPN
ATRX.HUMAN
CFAH_MOUSE
PCN3_SULTO
OPFP_YEAST
POLG_ECOIF
NQRF_NEIMB
SYQ_XYLFA
M3K4_HUMAN
Y331_MYCGE
GCTA_ACIFE
POLG_ECOIB
NGRF_REIMB
YB71_HAEIN
RRPL_AHSV9
SYE_MYCGE
GCTA_COEL
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077422;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Male-specific histanine-binding salivary protein precursor (MS-HBP)...
Rhipicephalus appendiculatus (Brown ear tick).
Eukaryota; Metazoa; Arthropoda; Chellcerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
NCBI_TaxID=34631;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

TISSUE-Salivary gland;

TISSUE-Salivary gland;

MEDLINE-9288454; PubMed-10360182;

Paesen G.C., Adams P.L., Harlos K., Nuttall P.A., Stuart D.I.;

"Tick histamine-binding proteins: isolation, cloning, and three-dimensional structure";

Mol. Cell 3:661-671(1999).

-i- FUNCTION: BINDS HISTAMINE WITH A HIGH-AFFINITY. THE ABILITY TO OUTCOMPETE HISTAMINE RECEPTORS INDICATES THAT ITS FUNCTION IS SUPPRESS INFLAMMATION DURING BLOOD FEEDING.
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### ALIGNMENTS

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PDB; 1QFV; 19-APR-00.
InterPro; IPR002970; His_binding.
Pfam; PF02098; His_binding; 1.
ProDom; PD152455; His_binding; 1.
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Female-specific histamine-binding protein 2 precursor (FS-HBP2
Rhipicephalus appendiculatus (Brown ear tick)
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
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MOI. Cell 3:661-671(1999).

-i- FUNCTION: BINDS HISTAMINE WITH A HIGH-AFFINITY. THE ABILITY TO OUTCOMPETE HISTAMINE RECEPTORS INDICATES THAT ITS FUNCTION IS SUPPRESS INFLAMMATION DURING BLOOD FEEDING.
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MEDLINE=99288454; PubMed=10360182;
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"Tick histamine-binding proteins: isolation, cloning,
dimensional structure.":
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MO1. Cell 3:661-671(1999).

- IFUNCTION: BINDS HISTAMINE WITH A HIGH-AFFINITY.

- OUTCOMPETE HISTAMINE RECEPTORS INDICATES THAT IT SUPPRESS INFLAMMATION DURING BLOOD FEEDING.

- I- SUBCELLULAR LOCATION: Secreted.
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TISSUE-Salivary gland;
MEDLINE-99288454; PubMed-10360182;
Paesen G.C., Adams P.L., Harlos K., Nuttall P.A., Stuart D.I.;
"Tick histamine-binding proteins: isolation, cloning, and three-
                                                                                                                                                                             EMBL; U96080; AAC63106.1; -. HSSP; 077421; 1QFT.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Female-specific histamine-binding protein 1 precursor (FS-HBP1
Rhipicephalus appendiculatus (Brown ear tick).
Eukaryota; Metazoa; Arthropoda; Chelicorata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                    s_binding; 1.
His_binding; 1
  187
166
                                                         18
190
                                                                                                                                                      His_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
  1.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 331.5; DB Pred. No. 7.5e-229; Mismatches 6:
                                                           POTENTIAL.
FEMALE-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6923A3E902552B6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190
                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                             HISTAMINE-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ITS
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HERESULF

ID AC

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OCCUPATION

OCCUPATI

S

SEQUENCE

190

**₹** 

21370

ME;

855BE151A90053B1

CRC64;

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RESULT 4

RS4_THEVO
ID RS4_T

AC Q8_TB9
DT 28-FE
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Best Local :
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                      EMBL; AP000992: BAB59704.1; -.
HAMAP; MF_01306; -; 1.
InterPro; IPR001912; Ribosomal_S4.
InterPro; IPR002942; S4.
InterPro; IPR002942; S4.
InterPro; IPR005710; S4_9_euk_arch.
Pfam; PF00163; Ribosomal_S4; 1.
Pfam; PF01479; S4; 1.
SMARP; SM00363; S4; 1.
TIGREAMS; TIGR01018; rpsD_arch; 1.
PROSITE; PS00632; RIBOSOMAL_S4; 1.
PROSITE; PS00632; RIBOSOMAL_S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequ
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanchori K., Kawamoto Nunoshiba T., Yamanoto Y., Aramaki H., Makino K., Suzuki M.; "Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium."; Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

-I- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 165 rRNA where it nucleates assembly of the body of the 30S subunit (By similarity).

-I- FUNCTION: With $5 and $12 plays an important role in translation.
                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed-11121031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPS4P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermoplasma volcanium. Archaea; Euryarchaeota; Thermoplasmata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RS4_THEVO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                accuracy (By similarity).

SUBUNIT: Part of the 30S ribosomal subunit. Contacts protein The interaction surface between $4 and $5 is involved in confort translational fidelity (By similarity).

SIMILARITY: Contains 1 $4 RNA binding domain.

SIMILARITY: BELONGS TO THE $4P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribosomal protein 54P.

o TY0562 OR TY0667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRNVYTDSSCKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
RNA-binding; rRNA-binding; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.0%; Score 267.5; 39.3%; Pred. No. 2.
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77;
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                                                                                                                                                                                                                                                                                                                                                                                                           Usage
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Best Local
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SEQUENCE
                                           DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRYBB.
                                                                                                GlycoSuiteDB; P26634; -...
InterPro; IPR001812; Trypan_glycop.
Pfam; PF00913; Trypan_glycop; 1.
Glycoprotein; Antigen; Trypanosomia
                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There extra the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variant surface glycoprotein MITAT 1.6 Trypanosoma_brucei brucei.
SEQUENCE
            LIPID
                                 CARBOHYD
                                                                                                                                                        EMBL; X56764; CAA40083.1;
                                                                                                                                                                                                                                                                                                                                               J. Mol.
                                                                                                                                                                                                                                                                                                                                                                    domains each having
                                                                                                                                                                                                                                                                                                                                                                                                     Carrington M., Miller N., Blum
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ISOlate MIAG 151;
MEDLINE-92046037; PubMed-1942032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Euglenozoa;
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P26334;
                                                                  PROPEP
                                                                              CHAIN
                                                                                        SIGNAL
                                                                                                                                             PIR; S18453; S18453
                                                                                                                                                                                                                                                                                                                                                            residues.
                                                                                                                                                                                                                                                                                                                                                                                "Variant specific glycoprotein of
                                                                                                                                                                                                                                                                                                                                                                                             Turner M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSM6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Attached A SOLUBLE FORM IS RELASED FROM PI-PLC.
                                                                                                                                                                                                                                                                                                               MOL. BIO1. 221:823-835(1991).
FUNCTION: VSG FORMS A COAT ON THE SURFACE OF TYPANOSOME EVADES THE IMMUNE RESPONSE OF THE A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRYBB_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -FEDVFVFSDYKNCDV------IFVPKERGSDEGDYELWVSED
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  529
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507
39
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22, Last sequence update)
40, Last annotation updat
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23161 MW;
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57284
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                                                                                                Trypanosomiasis;
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                              HYDROPHOBIC, REMOVED
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...
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Pred.
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          /FTId-CAR_000142.
GPI-ANCHOR (BY SIMILARITY).
                                                                            VARIANT SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                                     M. L.,
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  A1FB291B900502F4 CRC64;
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InterPro: IPR007087; Znf_C2H2
InterPro: IPR007087; Znf_C2H2
Pfam; PF00096; Zf-C2H2; 12.
ProDom; PD000003; Znf_C2H2; 1
SMART; SM00349; KRAB; 1.
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the Euro
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Z180_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2000)
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28-FEB-2003 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis gene cluster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Differential expansion of homologous zinc-finger human chromosome 19q13.2 and mouse chromosome 7."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shannon
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15-SEP-2003
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Local
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SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 KRAB
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                                                                                                                                                                                                                                                            non-profit institutions as long and this statement is not removed
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M., Branscomb
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                                                                                                                                                                                                                         equires a license agreement (S email to license@isb-sib.ch).
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation updat
c protein 180 (HHZ168).
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Best Local
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-cv. Little Marvel;
And L. Cohn N.S., Mitchell J.P.;
PA cDNA clone encoding a cell Wall invertase from pea.";
(In) Plant Gene Register PGF96-008.

-i- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing fractiofuranoside residues in beta-D-fructofuranosides.

-i- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing fractions of the control of t
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Q43089;
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CONFLICT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Beta-fructofuranosidase, cell wall isozyme pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZN_FING
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PROSITE;
PROSITE;
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(Sucrose-6-phosphate hydrolase) (Acid invertase).
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Pred. No. 5.7;
27; Mismatches
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-> W (IN REF. 2).
-> C (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable Ras-related protein Rab-4A.
Echinococcus multilocularis.
Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidea; Taeniidae; Echinococcus.
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PIR; T06491; T06491.
InterPro; IPR001362; Glyco_hydro_32.
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                                                                                                                                                                                                                                       J. Biol. Chem. 275:38311-38318(2000).
-I- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR TRAFFIC (BY SIMILARITY).
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Pfam; pF00251; Glyco_hydro_32; 1.

SMARF; SM00640; Glyco_32; 1.

PROSITE; PS00609; GLYCOSYL_HYDROL_F32;
                                                                                                                                                                                                                                                                                                                 "mRNA trans-splicing in the human parasitic cestode Echinococcus multilocularis.";
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                                                                                                                                                                                                                                                                                                                                                                        Brehm K., Jensen K.,
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20556267; PubMed-10973970;
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                                                                                                                                                                                                           TRAFFIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAB FAMILY.
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POTENTIAL.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
7B548E251CFD5D44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BETA-FRUCTOFURANOSIDASE, CELL WALL ISOZYME.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠.
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A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313
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                                                                                                                                    a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50;
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                           .ch/announce,
                                                                                                                                 outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                           9
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RESULT
C4BP_BC
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
16-OCT-2001
C4b-binding
                                                                                             This SWISS-PROT entry is copyright. It is produced through a celebrate the Ewiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-slb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                          C4BPA.
                                                                                                                                                                                                                                                                                                                                                                          C4BP_BOVIN
Q28065;
                                                                                                                                                                                                                                                                                                                                                                                              BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIPID
                                                                                                                                                                                                                                            TISSUE-Liver;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP-binding; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                MEDLINE=95015909; PubMed=7930621;
                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
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                                                                            SIMILARITY: TO C4BP E SIMILARITY: Contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                                                                                                                                                      171 LLSKVKSGELGADRLLVGSNK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 FVPKERGSDEGDYELWVSEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 ILYKNKHLTDLKESHETITVWKAYDYTTENGIKY-ETQGTRTQTFEDVFVFSDYKNCDVI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILVGNK -- KDLRDTDGQVTHWEANTFAQENGLQFIETSALTGENIDDAFT ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRO0231; small_GTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003579; GTPase_Rab.
IPR001806; Ras_trnsfrmng.
IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                      Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223
                                                                                                                                                                                                                                                                                                                                 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
protein alpha chain precursor (C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
64
122
38
221
223
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                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                            TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN Contains 8 Sushi (SCR) domains.
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                                                                                                                                                                                                                                                                                  Bos.
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68
125
46
221
223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.2%;
27.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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Pred. No.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     610
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                                                                                                                                                                                                                                                                                                                                   (C4bp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 223
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                                                  a collaboration -
MBL outstation -
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                                                outstation
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POS GRED DE AC
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OPPF_MYCPN
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Best Local S
Matches 32
                                                       OPPF_MYCPN STANDARD; PRT; 851 AA. P75551; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 011gopeptide transport ATP-binding protein oppoper OR MPN218 OR MP613.
Bacteria; Firmicutes;
NCBI_TaxID=2104;
[1]
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DOMAIN
                                          Mycoplasma pneumoniae
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PIR; I46001; I46001.
HSSP; P10998; IVVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00084; sushi; 8 SMART; SM00032; CCP; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro; IPR000436; Sushi_SCR_CCP
                                                                                                                                                                                                                                            434
                                                                                                                                                                                                                                                                         157
                                                                                                                                                                                                                                                                                                                                      132
                                                                                                                                                                                                                                                                                                                                                                   315
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                          VIAHGQHKVVSKFFT 448
                                                                                                                                                                                                                                                                                                                                                                HQTQTEQQVYDIGFVLSYKCHFGYKPETDGPTTVTCQSNLEWSPYIECKEVCCPEPNLNN
                                                                                                                                                                                                                                                                                                                                                                                            HETITVWKAYD-----YTTENGIKYETQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSD
                                                                                                                                                                                                                                                                      YFAQQQEKTYRNYYT
                                                                                                                                                                                                                                                                                                                                    EGDYEL-----WVSEDKID----
                                                                                                                                                                                                                                                                                                   YGSITLHRRPSTSTHCTYISGDKISYECHSKYMFDALCTKHGTWSPRTPECRPDCK-SPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610
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429
487
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                                                                                                                                                                                                                                                                                                                                                                                                                                               8.2%;
23.7%;
                           Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .asma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.
                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
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BY SIMILARITY.
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SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 6.
SUSHI 7.
SUSHI 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 81; DB
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
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                                                                           oppF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BETA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 610;
                                                                                                                                                                                                                                                                                                                                 -----KIPDC---CKFTMA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sushi; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                  374
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ATRX_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 44; Conserv
                                             Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
                                                                                                                                         ATEX_HUMAN STANDARD; PRT; 2492 AA. P46100; P51068; Q15886; Q9H0Z1; Q9NTS3; Q1-NOV-1995 (Rel. 32, Created)
28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Transcriptional regulator ATRX (X-11nked helicase nuclear protein) (XNP) (Znf-HX).
ATRX OR RAD54L OR XH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50093; ABC_TRANSPORTER_2; 1.
Peptide transport; Transport; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae.";

Nucleic Acids Res. 24:4420-4449(1996).

Nucleic Acids Res. 24:4420-4449(1996).

-I- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR OLIGOPEPTIDES. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE TRANSPORT SYSTEM (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Membrane-associated (Potential).

-I- SIMILARITY: Belongs to the ABC transporter family.
     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
NP_BIND 48
SEQUENCE 851 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=ATCC 29342 / MEDLINE=97105885; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000058; AAB96261.1; -. PIR; S73939; S73939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted [7]
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MCDOWell T.L., Gibbons R.J., Sutherland H., O'Rourke D.M.,
Bickmore W.A., Pombo A., Turley H., Gatter K., Picketts D.J.
Buckle V.J., Chapman L., Rhodes D., Higgs D.R.;
"Localization of a putative transcriptional regulator (ATRX)
pericentromeric heterochromatin and the short arms of acroce chromosomes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 860-2492 FROM N.A. MEDLINE-95179111; PubMed-7874112; MEDLINE-95179111; PubMed-7874112; MEDLINE-95179111; PubMed-7874112; MEDLINE-9517911; PubMed-7874112; MEDLINE-9517911; PubMed-7874112; MEDLINE-9517911; PubMed-7874112; MEDLINE-9517911; PubMed-7874112; PubMe
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WEDLINE-97123494; PubMed-8968741;

Picketts D.J., Higgs D.R., Bachoo Gibbons R.J.;
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MEDLINE-97196774; Povillard L., Lacombe
                                                                                                                                                              MEDLINE-20213147; PubMed-10751095;
                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Specific interaction between the XNP/ATR-X domain of the human EZH2 protein."; Hum. Mol. Genet. 7:679-684(1998).
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                                          ARIANT ATR-X SER-1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      one R.J., Picketts D.J., Villard L., Higgs D.R.; atlons in a putative global transcriptional regulator cause ed mental retardation with alpha-thalassemia (ATR-X syndrome 80:837-845(1995).
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helicase.";
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t S., Villard L.,
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XNP/ATR-X
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   the ATR-X syndrome.";
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S., Boncinelli E.,
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LEU-246 AND CYS-249.

MEDLINE-99219535; PubMed-10204841;

Villard L., Bonino M.-C., Abidi F., Ragusa A., Belougne J.,

Lossi A.-M., Seaver L., Bonnefont J.-P., Romano C., Fichera P.

Lacombe D., Hanauer A., Philip N., Schwartz C.E., Fontes M.;

Lacombe D., Hanauer A., Philip N., Schwartz C.E., Fontes M.;
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Bergoffen J., Berry S.A., Dahl N., Fryer
Levin M.L., Masuno M., Neri G., Pierpont
Higgs D.R.;
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MEDLINE-99347960; PubMed-10417298;
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-I- FUNCTION: COULD BE A GLOBAL TRANSCRIPTIONAL REC
                                                                                                                                                                                                                                                            "Evaluation of a mutation ATR-X syndrome.";
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MEDLINE-99326061; PubMed-10398237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mutations in transcriptional regulator ATRX establish the significance of a PHD-like domain."; nat. Genet. 17:146-148(1997).
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Munnich A., Lyonnet :
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AND CYS-1847.
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Am. J. Med. Genet. 85:249-251(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT ATR-X LEU-246
                                                              FUNCTION: COULD BE A GLOBAL TRANSCRIPTIONAL REGUI
GENE EXPRESSION BY AFFECTING CHROMATIN. MAY BE II
DEVELOPMENT AND FACIAL MORPHOGENESIS:
SUBUNIT: PROBABLY BINDS EXHZ. BINDS ANNEXIN V IN
PHOSPHATIDYLCHOLINE/PHOSPHATIDYLSERINE-DEPENDENT
                        similarity).
SUBCELLULAR LOCATION: !
HETEROCHROMATIN DURING
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INTERACTING
ALTERNATIVE
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mutation in a large fami
Genet. 12:359-360(1996).
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J., Mattei J.-F.,
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                                                                                                                                                                                                                     LEU-190;
                                                                                                                                                                                                                                                                                                                                                                                                                              Carpenter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family with Juberg-Marsidi syndrome.";
                                        NUCLEAR.
                       NUCLEAR. ASSOCIATED INTERPHASE AND MITC
                                                                                                                                                                                                                    ILE-194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.J., Aftimos S., Asenbauer B., Fryer A., Keppler K., Kurosawa ierpont M.E., Slaney S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                  from
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MANNER (By
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                                                                                                                                                                                                                                                                                                                                                           PRO-219;
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RESULT 12
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                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
02-FEB-2003 (Rel. 41, Last annotation update)
Complement factor H precursor (Protein beta-1-H).
                                                                                                                                                                                                  CFAH_MOUSE P06909;
     SEQUENCE FROM N.A
                                    NCBI_TaxID=10090;
                                                                                        Mus musculus (Mouse)
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                                                                                                           OR CFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: Defects in ATRX are the cause of Carpenter-Waziri syndrome (CWS), an X-linked recessive condition characterized by moderate mental retardation, short stature, brachlydactyly with excessive skin creases, and widening of the knuckles.

DISEASE: Defects in ATRX are the cause of Juberg-Warsidi syndrome (JW) [WIM:309590]. JM is a rare X-linked recessive disease characterized by severe mental retardation, growth failure, sensorineural deafness, microgenitalism and early death.

SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.

SIMILARITY: Contains 1 PHD-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Ubiquitous.

DISEASE: Defects in ATRX are the cause of X-linked alphathalasemia/mental retardation syndrome (ATR-X) [MIM:301040]. ATR-X is an X-linked disorder comprising severe psychomotor x is an X-linked disorder comprising severe psychomotor retardation, facial dysmorphism, urogenital abnormalities, and retardation, facial dysmorphism, urogenital abnormalities, and retardation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      paraplegia, microcephaly, short stature and cryptorchidism. DISEASE: Defects in ATRX are a cause of Smith-Fineman-Myers syndrome (SEM) [MIM:309580]. Clinical features include severe mental retardation, microcephaly, growth failure, facial anomalies and bilateral cryptorchidism. Due to the clinical overlap with ATR-X syndrome, some patients originally diagnosed as having SEM, might be affected by a variant of ATR-X syndrome which lack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erythrocyte inclusions.

DISEASE: Defects in ATRX are the cause of Sutherland-Haan mental retardation syndrome (SHS) [MIM:309470]. It is characterized by severe mental retardation with spastic characterized by severe mental retardation with spastic characterized by severe mental retardation with spastic characterized by severe mental retardation and counterpolations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hemoglobin h inclusions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retardation, facial dysmorphism, urogenital abnormalities, and alpha-thalassemia. An essential phenotypic trait are hemoglobin
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                                                                                                                                                                                                                                                                                                         SDGTEKLPEREEICHFPKGI-----KQIKNGTTDGEKK 1045
                                                                                                                                                                                                                                                                                                                                            EDKIDKIP---DCCKFTMAYFAQQQEKTVRNVYTDSSCK 176
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                                                       Rodentia;
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Pred. No. 71;
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InterPro; IPR000436;
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Natsuume-Sakai S., Nonaka M., Non
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MEDLINE-90148935; PubMed-2533512;
Munoz-Canoves P., Tack B.F., Vik D.P.;
Manalysis of complement factor H mRNA expression: dexamethasone
IFN-gamma increase the level of H in L cells.";
                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                     the European Bioinformatics Institute. The by non-profit institutions as long
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TISSUE SPECIFICITY: Synthesized by liver and secreted in POLYMORPHISM: TWO CODOMINANT ALLELES OF FACTOR H ARE PRESENTED TO THE PRESENT OF T
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s requires a license agreement (; an email to license@isb-sib.ch)
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                                                                                    is not removed
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CARBOHYD
                                             0973F5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
homolog C) (PCNA C).
PCNC OR ST0944.
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  Crenarchaeota;
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Thermoprote1;
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BY SIM
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Pred. No. 34;
13; Mismatches
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  Sulfolobales;
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  Sulfolobaceae
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PEP1_YEAST
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Best Local S
Matches 33
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[1]
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33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     190
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PEPI_YEAST STANDARD; PRT; 1579 AA.

p32319;

p1-0CT-1993 (Rel. 27, Created)

01-0CT-1993 (Rel. 27, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

Vacuolar protein sorting/targeting protein PEPI protein sorting receptor VPS10) (Carboxypeptidase sorting receptor VPS10) (Carboxype receptor).

Carboxypeptidase sorting receptor VPS10) (Carboxype receptor) (CPV receptor).

PEPI OR VPS10 OR YBL017C OR YBL0302 OR YBL03.22.

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sac Saccharomycetales; Sacchar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP000984; BAB65958.1; ..

HAMAP; MF_00317; -; 1.

InterPro; IPR000730; Pr_cel_nuc_antig.

Pfam; PF00705; PCNA; 1.

PRINTS; PR00339; PCNACYCLIN.

PRODOM; PD002673; Pr_cel_nuc_antig; 1.

PROSITE; PS01251; PCNA_1; FALSE_NEG.

PROSITE; PS01251; PCNA_2; FALSE_NEG.

PROSITE; PS01251; PCNA_2; FALSE_NEG.

DNA-binding; DNA replication; Complete proteome.

SEQUENCE 246 AA; 27436 MW; BA370A5D227B4E7F CRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21456156; PubMed=11572479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Res. 8:123-140(2001).

FUNCTION: Silding clamp subunit. Responsible catalytic subunit of DNA polymerase to DNA replication (By similarity).

SUBUNIT: Homotrimer (By similarity).

SIMILARITY: BELONGS TO THE PCNA FAMILY.
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; Pred. |
17; Mis
BLUJUA
Ker's Peast).
(; Saccharomycotina; Saccia
(; Saccharomyces.
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                                                                                                                                                                                                                                                                                       (Carboxypeptidase
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                                                                                                   Saccharomycetes
                                                                                                                                                                                                                                                                                                                                  precursor
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EMBL; Z35778; CAA84836.1; -.
EMBL; U07621; AAA18831.1; -.
PIR; S25329; S25329;
SGD; S0000113; PEP1.
GO; GO:0006623; P:protein-vacuolar targeting; IMGO; GO:0007034; P:vacuolar transport; IMP.
InterPro; IPR002860; GH_BNR.
InterPro; IPR002861; VPS10.
    CARBOHYD
CONFLICT
                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
NP_BIND
CARBOHYD
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                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02012; BNR; 13.
SMART; SM00602; VPS10; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-94243924;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oded by the VPS10 gene.";

1 77:579-586(1994).

1 PUNCTION: INVOLVED IN THE INTRACELLULAR SORTING AND DELIVERY OF SOLUBLE VACUOLAR PROTEINS, SEEMS TO SPECIFICALLY INTERACT WITH CARBOXYPEPTIDASE Y (CPY). MAY EXECUTE MULTIPLE ROUNDS OF SORTING BY CYCLING BETWEEN THE LATE GOLGI AND A PREVACUOLAR ENDOSOME-LIKE COMPARTMENT. BINDS THE GOLGI-MODIFIED P2 FORM OF CPY, AND THIS INVERACTION IS DEPENDENT ON THE PRESENCE OF AN INTACT CPY VACUOLAR PROTEIN SORTING SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPARTMENT.

DOMAIN: THE LUMENAL DOMAIN CONTAINS TWO REGIONS OF 650 AA THAT EXHIBIT 20% IDENTITY. THE CYTOPLASMIC DAS A GOLGI RETENTION/RECYCLING SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE PEP1 FAMILY OF MEMBRANE GLYCOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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orazdovsky B.F.,
N-LINKED (GLCNAC...) (PO)
T -> I (IN REF. 2).
D -> E (IN REF. 2).
G -> D (IN REF. 2).
AMNGSY -> SMYESR (IN REF. 2).
AMNGSY -> EKNISSRG (IN REF. 2).
QFE -> APV (IN REF. 2).
QFE -> A (IN REF. 2).
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S -> G (IN REF. 2).
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LUMENDAL (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
ATP (POTENTIAL).
N-LINKED (GLCNAC. . .) (PON-LINKED (GLCNAC. . .) (PON-LINKED (GLCNAC. . . ))
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VACUOLAR PROTEIN
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t arm of yeast o
ting gene PEP1,
                                                                                                                                                                                                                                (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; ATP-binding; Repeat
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SEQUENCE OF 570-853 FROM N.A.
SEQUENCE OF 570-853 FROM N.A.
MEDLINE-99138973; PubMed-9971773;
Oberste M.S., Maher K., Kilpatrick D.R., Pallansch M.A.;
Oberste M.S., Maher K., Kilpatrick D.R., Pallansch M.A.;
"Molecular evolution of the human enteroviruses: correlation
"Molecular evolution of the human enteroviruses: correlation
"Molecular evolution of the human enteroviruses: correlation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLG_ECOIF STANDARD; PRT; 2184 AA.

991734; Q66795; O9YID6;
15-JUL-199 (Rel. 38, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Coat protein VP4 (PlA); Coat protein VP1 (PlB); Picornail
(EC 3.4.22.29) (P2A); Core protein P2B; Core protein P2C; Core;
P3A; Genome-linked protein VP5 (P3B); Picornain SC (EC 3.4.22.2)

(Protease 3C) (P3C); RNA-directed RNA polymerase (EC 2.7.4.48)
EChovirus 1 (strain Farouk / ATCC VR-1038)
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                                                         MEDLINE-99192672; PubMed-10089900;
Filman D.J., Wien M.W., Cunningham J.A.,
                Acta Crystallogr. D 54:1261-1272(1998).
-!- FUNCTION: P2A AND THE P3C POLYPEPTIDES
                                          "Structure determination of echovirus
                                                                                                                                                                                                                                                                                    coxsackie B viruses.";
J. Gen. Virol. 77:715-725(1996).
                                                                                                                                                                                                                                                                                                                   "The major echovirus group
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Bergelson J.M.;
"Receptor interactions,
echovirus 1/8.";
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                                                                                       K-RAY CRYSTALLOGRAPHY (3.55 ANGSTROMS)
MEDLINE-99192672; PubMed-10089503;
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InterPro; IPR003593, AA_ATPASE.
InterPro; IPR003593, AA_ATPASE.
InterPro; IPR003138; Pico_PlA.
InterPro; IPR000199; Cys_protease_3C.
InterPro; IPR000199; Cys_protease_3C.
InterPro; IPR000181; Pico_PlA.
InterPro; IPR0002527; Pico_PlA.
InterPro; IPR0002527; Pico_PlA.
InterPro; IPR001676; RNA_Dell_PSD.
InterPro; IPR0017095; RNA_Dell_PSD.
InterPro; IPR0017095; RNA_Dell_PSD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: It is thought that the P2C protein attaches to vesicular membranes and is associated with viral RNA synthesis.

CATALYTIC ACTIVITY: Selective cleavage of Gln-|-Gly bond in the polivirus polyprotein. In other picornavirus reactions Glu may be substituted for Gln, and Ser or Thr for Gly.

CATALYTIC ACTIVITY: Selective cleavage of Tyr-|-Gly bond in the picornavirus polyprotein. In other picornavirus reactions Glu may be substituted for Gln, and Ser or Thr for Gly.

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL I EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VIVO3, AND VP4.

PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PLOTENANGE BETWEEN VP4 AND VP2 IS AUTOCATALYTIG; VP1/P2A IS CATALYZED BY PA5, ALL OTHER CLEAVAGES ARE CATALYZED BY PSIS ALL OTHER CLEAVAGES ARE CATALYZED BY PSIS ALL OTHER CLEAVAGES TO PEPTIDASE FAMILY C3.

SIMILARITY: P3A PROTEASE BELONGS TO PEPTIDASE FAMILY C3.

SIMILARITY: P3C PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
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         Core protein; Transferase; My:
; Hydrolase; Thiol protease;
COAT proTEIN VP4.
COAT PROTEIN VP2.
COAT PROTEIN VP1.
COAT PROTEIN VP1.
PICORNAIN 2A.
CORE PROTEIN P2B.
CORE PROTEIN P3A.
GENOME-LINKED PROTEIN VPG.
PICORNAIN 3C.
CORE PROTEIN B3A.
GENOME-LINKED PROTEIN VPG.
PICORNAIN 3C.
RNA-DIRECTED RNA POLYMERASE.
MYRISTATE.
PROTEASE 3C (POTENTIAL).
PROTEASE 3C (POTENTIAL).
N -> M (IN REF. 2).
N -> R (IN REF. 2).
                                                                                                                        JAN; Transferase; Myristate;
Jase; Thiol protease; 3D-structure
COAT PROTEIN VP4.
COAT PROTEIN VP2.
COAT PROTEIN VP3.
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| Search completed: August<br>Job time : 13.0933 secs | 170 Y<br>1212 Q                             | 116 x<br>1185 x   | 60 I<br>1125 Ç  | م 5<br>ا<br>1068   | Query Match<br>Best Local Sin<br>Matches 42;   | TURN HELIX TURN HELIX TURN HELIX TURN TURN TURN STRAND STRAND STRAND STRAND STRAND | THE CHECK |
| leted: Augus<br>13.0933 secs                        | 170 YTDSSCKPAP<br>   :  <br>1212 QFKSKCRIEP | YKNCDVIFV<br> <br>Y   | NATILYKN<br> <br> XFIEWLKV                                      | NEAKLGSY<br>  : <br>NTLALIGCT                              | =  | 4424<br>430<br>4430<br>4555  | נו        |
| ;t 1, 2003, 12:15:53                                | RP 179                                      | YKNCDVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEKTVRN-V 169<br> | 60 LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFSD 115 | ANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIGKKK 59 | 8.0%; Score 79.5; DB 1; Length 2184;<br>ilarity 22.1%; Pred. No. 82;<br>Conservative 24; Mismatches 73; Indels 51; Gaps 7; | 427<br>427<br>428<br>428<br>435<br>437<br>437<br>442<br>458<br>458                 |           |

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989
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Gapop 10.0 ,
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 Maximum Match 100%
Listing first 45 summaries
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| membrane nuclease   | C82885  | N | 434  | 7.7 | 76.5 | 45         |
|---------------------|---------|---|------|-----|------|------------|
| N-carbamyl-L-amino  | AE1500  | N | 414  | 7.7 | 76.5 | 44         |
| myosin heavy        | T18278  | N | 2245 | 7.8 | 77   | 43         |
| hypothetical        | T22147  | ພ | 2034 | 7.8 | 77   | 42         |
| probable transcri   | T38673  | N | 1108 | 7.8 | 77   | 41         |
| N, N-dimethylforman | JC7174  | N | 762  | 7.8 | 77   | 40         |
| trypomastigote sui  | S44237  | N | 719  | 7.8 | 77   | 39 .       |
| [od                 | S30483  | N | 656  | 7.8 | 77   | 38         |
| glutamate-tRNA lig  | A64251  | N | 484  | 7.8 | 77   | 37         |
| maltose/maltodext;  | C70038  | N | 421  | 7.8 | 77   | 36         |
| NAM-like protein    | T47983  | 2 | 334  | 7.8 | 77   | <u>3</u> 5 |
| translin associate  | T41566  | N | 231  | 7.8 | 77   | 34         |
| chromosome assemb   | 'в70356 | N | 1156 | 7.8 | 77.5 | ω<br>ω     |
| serine proteinase   | F89870  | N | 769  | 7.8 | 77.5 | 32         |
| N-carbamyl-L-amino  | AB1142  | N | 423  | 7.8 | 77.5 | 31         |
| hy                  | C64015  | N | 306  | 7.8 | 77.5 | 30         |

## ALIGNMENTS

hypothetical protein YDR267c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D9954.11
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 24-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 19-Apr-2002
C;Accession: S70127

submitted to the EMBL Data Library, May 1996
A;Description: The sequence of S. cerevisiae cosmid 9954
A;Reference number: S70124
A;Accession: S70127

R; Le,

RESULT 1 S70127

## A:Gene: MIPS:YDR267c A:Cross-references: SGD:S0002675 A:Map position: 4R Š 밁 Ş 밁 C;Superfamily: unassigned WD repeat proteins; WD repeat homology F;54-87/Domain: WD repeat homology <WD1>F;103-136/Domain: WD repeat homology <WD2>F;149-182/Domain: WD repeat homology <WD3> A;Molecule type: DNA A;Residues: 1-330 <LET> A;Cross-references: EMBL:U51030; NID:g1332633; PID:g1230640; GSPDB:GN00004; MIPS:YDR2 Matches Query Match Best Local Genetics: 165 114 69 16 AWKSLQQDQNKRYYLAQATQTTDGVW------GEEFTCVSVTAEKIGKKKLNATILYKN 38; Similarity VPKERGSDEGDYELWVSE 141 KHLTDLKESHETITVWKAYDYTTE-----NGIKYETQGTRTQTFEDVFVFSDYKNCDVIF 123 VWKYMGDDEDDQQEWVCE 242 EALLASSSYDDTVRIWKDYDDDWECVAVLNGHEGTVWSSDFDKTEGVFRLCSGSDDSTVR Conservative 11.5%; Score 113.5; 27.5%; Pred. No. 0. 17; Mismatches .016; გ ე Ņ Indels Length 330; 21; Gaps 164 68

two-component sensor histidine kinase lisk [imported] - Listeria monocytogenes (C;Species: Listeria monocytogenes (C;Species: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001 C;Accession: AB1247
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam

E.; Maitournam,

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RESULT AB1247

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RESULT 4
S18453
variant surface
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A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1609
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   C;Species:
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AF1609
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1247
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AL592022; PIDN:CAC96646.1; A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-483 <GLA>
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; Dominguez-Bernal, G.; Duc
D.; Jones, L.M.; Karst, U.
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AF1609
two-component sensor histidine kinase lisK [imported] - Listeria innocua (strain Clip11
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                                                                                                                      DEGDYELWVSEDKIDKIPDCCKFTMAYFAQQQEK 164
                                                                                                                                                    DTDLRALIQHNHLEQILIIIMDNAVKYSGDGTEV----DMHVYKEQKQIHI---
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Dussurget, O.; Entian, K.D.; Fsihi,
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Voss, H.; Wehland
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A; Title: Drosophila myoblast city encodes a conserved protein that is A; Reference number: Z14881; MUID:97392689; PMID:9245788 A; Accession: T03284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myoblast city protein - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 24-Mar-1999 *sequence_revision 24-Mar-1999 *text_ch C;Accession: T00284 R;Erickson, M.R.S.; Galletta, B.J.; Abmayr, S.M. J. Cell Biol. 138, 589-603, 1997
                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: mbc
A;Cross-references: FlyBase:FBgn0015513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X56764; NID:g10474; PIDN:CAA40083.1; C;Superfamily: variant surface glycoprotein C;Keywords: glycoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Carrington, M.; Miller, N.; Blum, M.; Roditi, I.; Wiley, D.
J. Mol. Biol. 221, 823-835, 1991
A;Title: Variant specific glycoprotein of Trypanosoma brucei A;Reference number: S18445; MUID:92046037; PMID:1942032
A;Accession: S18453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-1970 <E
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A; Residues: 1-529 < CAR>
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C;Accession: S18453
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553 VRLMQANGTTITQGQHILAVYKIDHKKYDKTVANCYLELPATVAELQ
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                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATRAKTDPYLQIWRAFKNLED----CESTFTSG-----
                                                                                                                                           ETQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KELKEAQEKATQANQN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKERGSDEGDYELWVSEDKIDKIPDCCKF------TMAYFAQQQEKTVR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANEAKLGSYQDAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNATI
                                                                                                                                                                                       EFARIAKTSE----KNVEVSVCVANEQGYLMPGVLSIGAGHQPIDEYKSVVYYHDDKPKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVYTDSSCKPAPA-QN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --KDGKDFYPQKLWDAMDKKDLLKDATQTNEIKKLADITDRSELNKVLLYYTRQKEQTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -YSRPSPETLKAADETKTAIK--NYVVQKEGKYD-QATDKE
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <ERI>
EMBL:AF007805;
                                                                                               -ETFKIHVPIEDFKQCHLRFVLKHRSSNE-----QKDRTEK---
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                                                                                                                                                                                                                                                                                                        Score 85.5;
Pred. No. 45;
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Pred. No. 7.8;
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                                              EKTVRNYYTDSSCKPAPAQ 181
                                                                                                                                                                                                                                                                                                                                   DВ
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A;Reference number: Z15715

A;Reference number: Z15715

A;Recession: T06491

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-555 <ZHA>

A;Cross-references: EMBL:X85327; NID:g1160487; PID:g773259

A;Experimental source: cv. Little Marvel

C;Genetics:
A;Note: bfruct1

C;Superfamily: beta-fructofuranosidase
C;Keywords: glycosidase; hydrolase
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C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein lmo0086 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AGI085 C;Accession: AGI085 Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Pominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T06491
R; Zhang, L.
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A;Cross-references: GB:NC_003210; PIDN:CAC98301.1; PID:g16409445; GSPDB:GN00177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, January 1996 A; Reference number: Z15715
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                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                 213 -AILYKSKNFVDWVEAKHPLHSAEGTGMWECPDFYPVLDKNLLRTGVDTSRNGDDDVRHV
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                        99
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                                                                                                         ATILYKNKHLTDLKE-----SHETITVWKAYDY------
                                                                                                                                                  PTIANKINSSSFRDPTTS-----WLGK-----DGFWR-----VLIGSKIDTKGM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVTAEKIG -- KKKLNATILYKNKHLTDLKESHET --- ITVWKAYDYTTENGIKYETQGTR 103
                   TQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSDEG---
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                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                     23.5%;
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Fsihi, H.
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N;Alternate names: cell wall invertase
C;Species: Plsum sativum (garden pea)
C;Date: 30-Apr-1999 #sequence_revision 3
C;Accession: T06380
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                                                                                                                                                                                                                               A;Gene: L1
C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                A; Title: Functional A; Reference number: A; Accession: T00494
                                                                                                                                                                                                                                                                                                                                                                                                                                             R;van der Lende, T.R.; Duitman, E.H.; Gunnewijk, M.G.W.; Yu, L.; Wessels, J.G.H. Virology 217, 88-96, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA-directed RNA polymerase (EC 2.7.7.48) - white button mushroom virus 1 N;Alternate names: RNA-dependent RNA polymerase C:Species: white button mushroom virus 1 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: cv.
C;Genetics:
A;Gene: bfructl
C;Function:
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A; Accession: T06380
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                                                                                                                                                                                                                                                                             C;Genetics:
                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: X94361;
                                                                                                                                                                                                                                                                                                                                                            A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                               53 ALSNINPDDNAPFIFVQTCELAEAI-GVQIAMVLIVKEGI----IQQTDRYKSLSREEQK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ATILYKNKHLTDLKE-----SHETITVWKAYDY------
                                                                                                       16 AWKSLOODQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNATILYKN-----
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--KHLTDLKESHETITVWKAYDYT-----TENGIKYETQGTRTQTFEDVFVFSDYKNCDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKVSLDDTKHDHYLIGSYDVVKDVFVPENGFEDNGFVLRYDY 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSDEG----
                                                                                                                                                  Conservative
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MBL Data Library, May
                                                                                                                                                                                                                                                                                                                                                                                                    analysis of dsrNAs (L1,L3, L5 and M2) associated with isometric 214158; MUID:96177126; PMID:8599239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL:AF063246; NID:g3152879; ce: cv. Little Marvel
                                                                                                                                                                8.48;
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                                                                                                                                                33;
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Pred. No. 13;
22; Mismatches
                                                                                                                                                Score 83.5; D
Pred. No. 32;
33; Mismatches
                                                                                                                                                                                                                                                                                                 NID:g1217917; PIDN:CAA64144.1;
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                                                                                                                                                71;
                                                                                                                                                                                        <u>ب</u>
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                                                                                                                                                                                        Length 1078;
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                                                                                                                                                39;
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                                                                                                                                                Gaps
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212

121

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hypothetical protein PFB0375w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence remission
                                                                                       G71616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390, 249-256, 1997

A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanloon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serora akeuchi, M.; Tamakoshi, A.; Tanamoto, H.; Yamane, K.; Yasumoto, K.; Yata, Y.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Arithors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; A; Accession: A69914

A; Status: nucleic acid sequence not shown; translation not shown

A. Molocule true. Nax
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R;Lazarevic, V.; Duestarhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karame submitted to the EMBL Data Library, August 1997
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025535; PIDN:AAC13030.1
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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A; Residues: 1-306 <LAZ>
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Best Local
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37; Conserv
                                                                                                                                                                                                                                                                                                         KSTEDI ---- SKEDIDELMQFWGRGLDVEDY - IWLQNEYID ----- FTNRYECDSKGM 174
                                                                                                                                                                                                                                                                                                                                                            QTFEDVFVFSDYKNCDVIFVPKERGSDEGDYELWVSEDKIDKIPDCCKFTMAY-----
                                                                                                                                                                                                                                                                                                                                                                                                                  VSAVNESESKKKSAGNVLGTYMKNIGMKDYKSK-----TWADSEFDFEEEQEYTTQLLLA 126
                                                                                                                                                                                             ELLINEICLTRLDIRKRRENGEKYDQQQKTLQDLLGSSNLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSVTAEKIGKKKLNATIL---YKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRT 104
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Pred. No. 8;
                                                                                                                                                                                                                                                   FAQQQEKTVENVYTDSSCKP 177
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  #text_change
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                                                                                                                                                                                                216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
  21-Jul-2000
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RESULT 13
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A;Cross references: EMBL:231693; NID:g469117; PIDN:CAA83498.1; PID:g469118 C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat F;50-107/Domain: complement factor H repeat homology <FH1> F;112-169/Domain: complement factor H repeat homology <FH2> F;174-234/Domain: complement factor H repeat homology <FH3> F;239-294/Domain: complement factor H repeat homology <FH4> F;29-362/Domain: complement factor H repeat homology <FH5> F;366-425/Domain: complement factor H repeat homology <FH6> F;369-362/Domain: complement factor H repeat homology <FH6> F;369-483/Domain: complement factor H repeat homology <FH8> F;489-483/Domain: complement factor H repeat homology <FH8>
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule 1-1802 <GAR>
A;Cross-references: GB:AE001390;
A;Cross-references: Clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hillarp, A.; Thern, A.; Dahlback, B.

J. Immunol. 153, 4190-4199, 1994
A;Title: Bovine C4b binding protein. Molecular cloning A;Reference number: 146001; MUID:95015909; PMID:7930621
A;Accession: 146001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, ; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: G71616
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A; Residues: 1-610 <HIL>
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                                                                                                                                                132 EGDYEL------WVSEDKID-----
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                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                   Similarity
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                                             YFAQQQEKTVRNVYT 171
VIAHGQHKVVSKFFT
                                                                                                                                                                                                                                         HETITVWKAYD-----YTTENGIKYETQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSD 131
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                                                                                                YGSITLHRRPSTSTHCTYISGDKISYECHSKYMFDALCTKHGTWSPRTPECRPDCK-SPP
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25.9%; Pred. No. 74;
                                                                                                                                                                                                                                                                                            14;
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                                                                                                                                                                                                                                                                                         Score 81; DB
Pred. No. 26;
14; Mismatches
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                                                                                                                                                                                                                                                                                                                                         Length 610
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                                                                                                                                         ----KIPDC---CKFTMA 156
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                                                                                                                                                                                                                                                                                         42;
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polyprotein

human

immunodeficiency

virus

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C;Genetics:
A;Genetics:
A;Genetic oppF
A;Genetic code: SGC3
A;Genetic code: SGC3
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology C;Keywords: ATP; nucleotide binding; P-loop
F;31-764/Domain: ATP-binding cassette homology #status atypical <ABCL>
F;48-55/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasm A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73939
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                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-851 <HIM>
A;Residues: 1-851 <HIM>
A;Cross-references: EMBL:AE000058; GB:U00089; NID:g1674291; PIDN:AAB96261.1; PID:g167431
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
573939
colligopeptide transport ATP-binding protein oppF - Mycoplasma pneumoniae (strain ATCC N;Alternate names: hypothetical protein G07_orf851
c;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
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C;Superfamily: pol polyprotein
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A;Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: human immunodeficiency virus type 2, HIV-2
C:Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 23-Mar-2001
C:Accession: S30484
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C;Accession: S73939
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A; Accession: S30484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                     Query Match
Best Local S
Matches 44
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Best Local S
Matches 42
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nes 42; Conserv
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                                                                                                                                                                     Similarity 23.7
14; Conservative
                          ---LNATILYKNKHLTDLKESHETITVWKAYDYTTENGIKYETQGTRTQTFEDVFVFS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPKERGSDEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLKELLNDLGFLTPEEKFQKDPPYHWMGYELWPTKWKLQKIE-----LPQREDWTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KESHETITVWKA----YDYTTENGI----KYETQGTRTQTFEDVFVFSDYKNCD---VIF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAWKSLQQDQNKRYYLAQATQTTDGVWGEEFTCVSVTAEKIGKKKLNATILYKNKHLTDL 74
                                                                                  TTOOKAKVSTOAFATWOKLOOTKONLKAYRAO
                                                                                                                           TWANEAKLGSYODA-WKSLOO-DONKRYYLAQATQTTDGVWGEEFTCVSVTAEKIGKKK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDI 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQG-----WKGSPAIFQYTMRNVLEPFRKANSDVTLIQYMDDILIASDRTDLEHDKVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAYFSIPLDEEFRQYTA------FTLPSVNNAEPGKR-----YIYK-----VL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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23.7%;
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                                                                                                                                                                       26;
                                                                                                                                                                   Score 81; DB:
Pred. No. 39;
26; Mismatches
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Pred. No.
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                                                                                                                                                                                                                DB 2;
-TTKNYIKDSRQ--NTQLTDDVFAFSYND
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                                                                                  -MAEELQNKPR
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C;Accession: I38614

R;Stayton, C.L.; Dabovic, B.; Gulisano, M.; Gecz, J.; Broccoli, Hum. Mol. Genet. 3, 1957-1964, 1994

A;Title: Cloning and characterization of a new human xq13 gene, A;Reference number: I38614; MUID:95179111; PMID:7874112

A;Accession: I38614
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I38614
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A;Molecule type: mRNA
A;Residues: 1-1641 <RES>
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C; Date: 29-May-1998 #sequence
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                                                                                                                                                                                                                     54 QASASTDGVDKLSGKEQSFTSLEVRKVAETK-----EKSKHL------KTKTCKKVQD 100
                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                 GLSDIAEKFLKKDQSDETSED-----DKKQSKKGTEEKKKPSDFKKKVIKMEQQYE--SS
                                                                                                                                                                                 YTTENGIKYETQGTRTQTFEDVFVFSDYKNCDVIFVPKERGSD------EGDYELWVS 140
                                                                                                                                                                                                                                                       QATQTTDGV---WGEEFTCVSVTAEKIGKKKLNATILYKNKHLTDLKESHETITVWKAYD 88
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                                                                         SDGTEKLPEREEICHFPKGI-----KQIKNGTTDGEKK 186
                                                                                                           EDKIDKIP---- DCCKFTMAYFAQQQEKTVRNVYTDSSCK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVDKKRRLVLVLSEYYKALPYFYDNWIHQNADRFDELTNAVFFDLIDVVIALNRDFANVE 386
                                                                                                                                                                                                                                                                                            Conservative
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                    2003, 12:16:36
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Pred. No.
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